

Query Match	Best Local Similarity	100.0%;	Score 2822;	DB 6;	Length 2822;	Mismatches	Indels	Gaps
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ACCESSION	AX549232	DEFINITION	Sequence 517 from Patent WO02061087.				
VERSION	AX549232.1		GI:25813927				

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.

**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**

Burnier, G.C., Roush, C.L. and Brown, J.P.  
Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides  
Patent: WO 02061087-A 517 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)

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Query Match	100.0%;	Score 2822;	DB 6;	Length 2822;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2822;	Conservative	0;	Mismatches	0;
			Indels	0;
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ACCESSION AF106858  
VERSION .AF106858.1 GI:4836764  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Liu, M., Parker, R.M., Darby, K., Byrne, H.J., Copeland, N.G., Crawford, J., Gilbert, D.D., Sutherland, G.R., Jenkins, N.A. and Herzog, H.  
TITLE GPR56, a novel secretin-like human G-protein-coupled receptor gene  
JOURNAL Genomics 55 (3), 296-305 (1999)  
MEDLINE 99168899  
PUBMED 10049584  
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AUTHORS Herzog, H.  
TITLE Direct Submision  
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ORIGIN

Query Match 100.0%; Score 2822; DB 9; Length 2822;  
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 Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
AX029424 2834 bp DNA linear PAT 16-SEP-2000  
LOCUS AX029424  
DEFINITION Sequence 4 from Patent WO915551.

ACCESSION AX029424  
VERSION AX029424.1 GI:10190217  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
1 Herzig, H.  
TITLE Novel receptor  
JOURNAL Patent: WO 915551-A 01-APR-1999;  
GARVAN INST MED RES (AU) ; HERZOG HERBERT (AU)  
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ORIGIN  
Query Match 100.0%; Score 2822; DB 6; Length 2834;  
Best Local Similarly 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGACGAGGAGTCTGCTGTGTCAACAGGCTGAGTGTGATCTTGGCTCAT 60  
DB 7 CGGACGAGGAGTCTGCTGTGTCAACAGGCTGAGTGTGATCTTGGCTCAT 66  
QY 61 CGTAACTTCACTCCGAGTTCAAGTATCTTCAAGCTTCCAGTATGCTGGG 120  
DB 67 CGTAACTTCACTCCGAGTTCAAGTATCTTCAAGCTTCCAGTATGCTGGG 126  
QY 121 ATTACAGTGTGATCTTCAAGGAGTGTGCTCGTGGAGGAAATGACTCCCAAGTCTG 180  
DB 127 ATTACAGTGTGATCTTCAAGGAGTGTGCTCGTGGAGGAAATGACTCCCAAGTCTG 186  
QY 181 CTGACAGAGCACTGTGTCTGTGTGAGTGTCTTCTGTGTCAAGGCTGCAAGGCTG 240  
DB 187 CTGACAGAGCACTGTGTCTGTGTGAGTGTCTTCTGTGTCAAGGCTGCAAGGCTG 246  
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DB 367 GTCCATGCCCCCTTTCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 426  
QY 421 CTGACAGCTTGTGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 480  
DB 427 CTGACAGCTTGTGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 486  
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Db 1267 GAGACCTGTCAG 1326  
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RESULT 5  
BD062446  
LOCUS BD062446 2834 bp DNA linear PART 27-AUG-2002

DEFINITION Novel receptor.  
 ACCESSION BD062446  
 VERSION BD062446.1 GI:22608049  
 KEYWORDS JP 2001513653-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eultheria; Primates; Carnivora; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 2834)  
 AUTHORS Herzog, H.  
 TITLE Novel receptor  
 JOURNAL Patent: JP 2001513653-A 2 04-SEP-2001;  
 GARVAN INSTITUTE OF MEDICAL RESEARCH  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001513653-A/2  
 PD 04-SEP-2001  
 PR 24-SEP-1998 JP 1999518348  
 PR 24-SEP-1997 AU PO 9386  
 PI HERBERT HERZOG  
 PC C07K7/06, C07K14/705, C07K16/28, C12N15/12, C12N5/10, C12P21/02, PC A01K67/027, G01N33/68, C07H21/04  
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 Qy 127 ATTACAGGTGAGCTTCCAGAGTGAATCGGTGAGAGAAATGATCCCAAGCGCTG 186  
 Db 181 CTGACAGAGCACTGTCTCTGTGAGTGTCTTCTGTGCAAGTGGCCACGGCAAG 240  
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QY	1801	TTGGCTGTGCATATGAGACTCCAGAGGGGCTGTATCTTACCTTCCATGTGTGCATATCCGGGAC	1860
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QY	1861	TTCCCTGTGCATACATCATCAACACTTGGGCTCTTCCAGCCTGTGTGTTTCTGTTCACATG	1920
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QY	1921	GCCATGTGACCACTATGTGTGTGCAGATCTCTGGGCTGTGGGCCCCCAACCCAAAATGTG	1980
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Db	1987	TTCAATATGTGCATACATGCTGTGGGCTCAGGCTGTGCTTGGGCTGTGCGCTGTATGTC	2046
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QY	2221	AGCACTCTGTCCAGCCGCTCTAGAGGCTCTCAGCCCTCAGCCTGTGCCATGTGTGAAGCAGAGA	2280
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QY	2521	CCAGCTGAGAGGCTGTGTCTCTCTTTCACAACCCTGTGGGCCAGGCTCATTTGCTGGGGGCTCA	2580
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Db	2707	TTTTTAACCTCAGATGGACACCGAGGGCGAATGGGGCCGAGGGACAGACTTTCAGGGCCAGAG	2766

Qy	2761	CCCTGCGCGAGGAGGAGGCGCCCTTTGGCCAGAGGACACAGAGAGCTGCGCTACCTGTAGGCC	2820
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Qy	2821	CG 2822	
Db	2827	CG 2828	
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LOCUS	CG412946	3902 bp	DNA
DEFINITION	Sequence 20017 from Patent WO0170979.	linear	PAT 23-JAN-2004
ACCESSION	CG412946		
VERSION	CG412946.1	GI:41320727	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1		
AUTHORS	Lee, J. and Millie, J.		
TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer		
JOURNAL	Patent: WO 0170979-A 20017 27-SEP-2001;		
	Millennium Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
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Best Local Similarity	99.7%;	Fred. No. 0;	
Matches 2812; Conservative	0;	Mismatches	6; Indels 3; Gaps 2
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Db	304	GGCAGCAGAGGCTCGCTCTGTCAACAGAGCTGAGTGCAGGTGTGATCTTTGGCTCATC	363
Qy	62	GTAACTTCCACTCCCGGGGTTCAAGTATTTCTCAGTCCCTCAAGCCCTCCGAGTATGGGA	121
Db	364	GTAACTTCCACTCCCGGGGTTCAAGTATTTCTCAGTCCCTCAAGCCCTCCGAGTATGGGA	423
Qy	122	TTACAGGTGTGATCTTCCAGAGTACTCCGTCGAGGAAATATGACTCCCAAGTCCTGC	181
Db	424	TTACAGGTGTGATCTTCCAGAGTACTCCGTCGAGGAAATATGACTCCCAAGTCCTGC	483
Qy	182	TGCAGACGACACTGTTCTCTGTAGTGTGCTCTTCTTGTCCTCAAGTGTCCACGGCAGG	241
Db	484	TGCAGACGACACTGTTCTCTGTAGTGTGCTCTTCTTGTCCTCAAGTGTCCACGGCAGG	543
Qy	242	GGCAGCAGGGAACCTTGGCTTCTCAAGCAGCGGAAACAGACACACAGAGCAGCCTCC	301
Db	544	GGCAGCAGGGAACCTTGGCTTCTCAAGCAGCGGAAACAGACACACAGAGCAGCCTCC	603
Qy	302	ACTACAAACCCACACACAGACTGCGGATCTCCATCGAGAACTCCGAGAGGCCCTTCAAG	361
Db	604	ACTACAAACCCACACACAGACTGCGGATCTCCATCGAGAACTCCGAGAGGCCCTTCAAG	663
Qy	362	TCCATGCCCTTTTCCCTGACGCCACCTCTGTTCCGATTCCTTCCCTGACCCGAGGGCC	421
Db	664	TCCATGCCCTTTTCCCTGACGCCACCTCTGTTCCGATTCCTTCCCTGACCCGAGGGCC	723
Qy	422	TCTACACATTTGCGCTCTTACTGGAACCGACATGCTGGAGATTACATCTTCTTATGGCA	481
Db	724	TCTACACATTTGCGCTCTTACTGGAACCGACATGCTGGAGATTACATCTTCTTATGGCA	783
Qy	482	AGCGTACATTTGTGAGTGAACAAGCCTTAGCCTCCTTGTCTTCCAGACCAAGAGG	541
Db	784	AGCGTACATTTGTGAGTGAACAAGCCTTAGCCTCCTTGTCTTCCAGACCAAGAGG	843

QY	542	AGAGCCTGGCTCAGAGGCCCCCGCTGTTAGCACTTGTGACACTCTCTGCTGGAGAGCCCTC	601
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QY	602	AGAACATCAGGCTGCGCAGATGCGCCAGACTTCACTTCTCTTCCAGAGTCTTCCACCA	661
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QY	662	CGGCGGCTCACATGCTCGGTGGACATGTGCGAGCTCAAAAGGAACTTCACTGCTTCA	721
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QY	842	CCTTCGAGAGAGACCGGATTCAAACCCACACGTATGAAAGCTCAGCCCAAGCGGAGCTCC	901
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Db	1204	AGGACCTGCAATCCACTCCGGAGAGAGAGAGAGGAGATCATATGAGTACTCGG	1263
QY	962	TGCTGCTGCTCTGAAACACTTTTCCAGAGAGCAAAAGGCCGAGAGCGGGAGGCTTAAGA	1021
Db	1264	TGCTGCTGCTCTGAAACACTTTTCCAGAGAGCAAAAGGCCGAGAGCGGGAGGCTTAAGA	1323
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Db	1324	GACTCCTCCTGATGACTTTCAGCAGCCAGCCCTGTTCCAGAGCAAGATTCAGCCAG	1383
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QY	1262	AGACCGTCAAGAGAAACCAAAATATCTGTCTTGTGAACCACTGTGACCTTATTTGAG	1321
Db	1564	AGACCGTCAAGAGAAACCAAAATATCTGTCTTGTGAACCACTGTGACCTTATTTGAG	1623
QY	1322	TGCTGATGATCTCCTCGGTGAGAGTGAACGCCGTGCAAGAGCACTTACGTAGCCTCT	1381
Db	1624	TGCTGATGATCTCCTCGGTGAGAGTGAACGCCGTGCAAGAGCACTTACGTAGCCTCT	1683
QY	1382	CCTAAGTGGGCTGTGTCTTCTTGCCCTGAGCTGCTTGTACCACTTGTGCGCTTACCT	1441
Db	1684	CCTAAGTGGGCTGTGTCTTCTTGCCCTGAGCTGCTTGTACCACTTGTGCGCTTACCT	1743
QY	1442	GCTTCAGGAGTGCCTCGCTGAGAGAACTCGGAGCTACACATCAAGATGAGCA	1501
Db	1744	GCTTCAGGAGTGCCTCGCTGAGAGAACTCGGAGCTACACATCAAGATGAGCA	1803
QY	1502	TGAACCTGTGCTGTGCGCTTCTTCTGTGTGGAACAAGACTTCTGTCTCAGCGAGCGGTG	1561
Db	1804	TGAACCTGTGCTGTGCGCGCTTCTTCTGTGTGGAACAAGACTTCTGTCTCAGCGAGCGGTG	1863
QY	1562	CCCTGACAGGCTCTGAGGCTGTGGCTGGCGAGGACAGTGCATCTTCTGCACTTCTCCCTG	1621
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Db	1984	TCCTTTGGACAATAATGTCCCGGCTTACTCAAGCTGAGCGCCANAGGGCTGGGACTTCC	2043
Oy	1742	CCATCTTTCTGTGAGAGCTGTGTGCCCTGTGTGAGATGTGAGCAACATAAGCCCCCATCATCT	1801
Db	2044	CCAATCTTCTGTGTGAGAGCTGTGTGCCCTGTGTGAGATGTGAGCAACATAAGCCCCCATCATCT	2103
Oy	1802	TGGCTGTGCATATAGAACTCCAGAAGGAGGTATCAACCCTTCAATGTGCTGGAATCCGGAGCT	1861
Db	2104	TGGCTGTGCATATAGAACTCCAGAAGGAGGTATCAACCCTTCAATGTGCTGGAATCCGGAGCT	2163
Oy	1862	CCCTGTGACGCTACATCAACAACCTTGGGCTCTTCAAGCCTGTGTGTTCTGTTCACATAG	1921
Db	2164	CCCTGTGACGCTACATCAACAACCTTGGGCTCTTCAAGCCTGTGTGTTCTGTTCACATAG	2223
Oy	1922	CCAGTGAAGCACCAATGGTATGATGATGCTGTGAGCTGAGGCCCAACACCAAATGTGT	1981
Db	2224	CCAGTGAAGCACCAATGGTATGATGATGCTGTGAGCTGAGGCCCAACACCAAATGTGT	2283
Oy	1982	CACATGTGTGACACATGCTGTGGGCTCAAGCCTGTGTCTTGGGCTGCTTGGGCTTTATCT	2041
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Db	2344	TCCTTCTCCTTGTGCTTCTGTGCAACCTTCCAGGTATGTGTGCTCTACCTTTTCAGCATATCA	2403
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Db	2404	CCCTCCTTTCAGAGCTTCTCTATCTTCACTGTGTATCTGTATCATGTGCTCATGTGCGGCTTCCAGGCCGG	2463
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Db	2464	GTCGCCCCTCCCTCTCTGTAAGGCACTCAACCTGTGCGGCAAGGCTCCCATCAGCTCGGAGCA	2523
Oy	2222	GCACCTGGTCCAGGCGGATCTAAGGCTCTCAAGCCACCTGTGCCATGTGTATGATAGACAGAT	2281
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ACCESSION CQ768015  
VERSION CQ768015.1 GI:45108767  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Wood, W. I., Goddard, A., Gurney, A., Yuan, J., Baker, K. P. and Chen, J.  
Human neurotrophin homologue  
Patent: EP 1386931-A 482 04-FEB-2004;  
JOURNAL Genentech, Inc. (US)  
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ORIGIN  
Query Match 98.6%; Score 2783.4; DB 6; Length 3819;  
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Qy 4 CAGCAGGAGTCTCGCTGTGTACACAGGCTGAGTGCAGTGTGATCTTGGCTCATCGT 63  
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Qy 64 AACCTCAGCTCCCGGGTTCAAGTATTCATCCTCAGCTCCGAGTACCTGGATTT 123  
Db 115 AACCTCAGCTCCCGGGTTCAAGTATTCATCCTCAGCTCCGAGTACCTGGATTT 174  
Qy 124 ACAGGTGTGATCTTCCAGAGTGACTCCGTCGAGGAAATGATCCCGAGTCCGCTG 183  
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DEFINITION Sequence 405 from patent US 6725730.  
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VERSION AR528654.1 GI:53916732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3819)  
AUTHORS Bollinger, C.L. Jr.  
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JOURNAL Patent: US 6725730-A 405 27-Apr-2004;  
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Oy	784	CAGTTGCAAGACCTGAGAGTCGAAACTGACCTCTGTGAGATTCAATGGGGGACATATGATGCC	843
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Db	1255	TTCTGAGGTGAAGACCCCAATGAGACAGCCCGGAGCATTTGAGACAGTGTGAGTGTGAG	1314
Oy	1264	ACCCTCAGAGAGAAACCCAAACATCTGCTTCTTGCAACACTTGACCTTATTTGCAATG	1323
Db	1315	ACCCTCAGAGAGAAACCCAAACATCTGCTTCTTGCAACACTTGACCTTATTTGCAATG	1374
Oy	1324	CTGATATGTTCTCTCGGTGAGAGTGGAGCCCGTGGACAAAGACATCACTGAGGCTCTCTCC	1383
Db	1375	CTGATATGTTCTCTCGGTGAGAGTGGAGCCCGTGGACAAAGACATCACTGAGGCTCTCTCC	1434
Oy	1384	TACGTGAGCTGTGTGCTCTGACCCTGAGCTTGTACACATTTGCGGCTCACTCTGTC	1443
Db	1435	TACGTGAGCTGTGTGCTCTGACCCTGAGCTTGTACACATTTGCGGCTCACTCTGTC	1494
Oy	1444	TTCAGGTTGCCCTTGCCTGCTGACGAGAGAAACCTCGGACATCAACATTAAGTGTCAATG	1503
Db	1495	TTCAGGTTGCCCTTGCCTGCTGACGAGAGAAACCTCGGACATCAACATTAAGTGTCAATG	1554
Oy	1504	AACCTGCTGAGCGGCTCTTCTGCTGACGACGAACTTCTGAGTCTCAGCGAGACCGGTGAGC	1563
Db	1555	AACCTGCTGAGCGGCTCTTCTGCTGACGACGAACTTCTGAGTCTCAGCGAGACCGGTGAGC	1614
Oy	1564	CTGACAGGCTCTGAGGCTGAGCTGACCGAGCTCAATGTCATTTCTCTGCTGCTC	1623
Db	1615	CTGACAGGCTCTGAGGCTGAGCTGACCGAGCTCAATGTCATTTCTCTGCTGCTC	1674
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Db	1675	AACCTGCTTTCCTGATGAGGCTCCGAGGGGTACAACCTTACCGACTGATGATGAGGCTC	1734
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Db	1735	TTTGGCACTTATGTCCTCGGCTACCTACTCAAGCTGAGGCCAATGGGCTGGGGCTTCC	1794
Qy	1744	ATCTTTGAGGAGCGCTGCTGGCCCTGGTGGATGAGCACTATGGCCCATCATCTTG	1803
Db	1795	ATCTTTCTGGTGAACGCTGCTGGCCCTGGTGGATGAGCACTATGGCCCATCATCTTG	1854
Qy	1804	GCTGTGATAGGACTCTCAGAGGGGCTCATCTAACCTTCCATAGTGTGGATCCGGGACCTC	1863
Db	1855	GCTGTGATAGGACTCTCAGAGGGGCTCATCTAACCTTCCATAGTGTGGATCCGGGACCTC	1914
Qy	1864	CTGTGACACTCATATCAACAACCTGGGGCTCTTCAGCCTGATGTTCTGTTCAACATGACC	1923
Db	1915	CTGTGACACTCATATCAACAACCTGGGGCTCTTCAGCCTGATGTTCTGTTCAACATGACC	1974
Qy	1924	ATGTAGCACCACTAGTGGTGCAGATCTCGGGCTGGCCGCCCCACACCCCAAAAGTGTC	1983
Db	1975	ATGTAGCACCACTAGTGGTGCAGATCTCGGGCTGGCCGCCCCACACCCCAAAAGTGTC	2034
Qy	1984	CATGTGCTGACACTGCTGGGGCTCAGCCTGGCTCTTGGCCCTGGCCCTGGATCTTCTTC	2043
Db	2035	CATGTGCTGACACTGCTGGGGCTCAGCCTGGCTCTTGGCCCTGGCCCTGGATCTTCTTC	2094
Qy	2044	TTCTCTCTTGGCTCTGGGACCTTCCAGCTTGTCGTCCTTCACTCTTTCAGCATCATCAC	2103
Db	2095	TTCTCTCTTGGCTCTGGGACCTTCCAGCTTGTCGTCCTTCACTCTTTCAGCATCATCAC	2154
Qy	2104	TCTTTCAGAGGCTCTCTCATCTTCACTTGGTATCGGTGCATGGGCTGCAGGCCCGGGGT	2163
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Qy	2164	GGCCCTCTCCCTCTGTAAGAGCACTTCAGCTGCGCCAGGCTCCCATCAGCTCTGGGACAC	2223
Db	2215	GGCCCTCTCCCTCTGTAAGAGCACTTCAGCTGCGCCAGGCTCCCATCAGCTCTGGGACAC	2274
Qy	2224	ACCTGTTCAGCGCGCACTTAGGCTCTCAGCCCACTGCCCATGTGATGAAGCAGAGATGC	2283
Db	2275	ACCTGTTCAGCGCGCACTTAGGCTCTCAGCCCACTGCCCATGTGATGAAGCAGAGATGC	2334
Qy	2284	GGCTCTGTGCACACTGCTGTGGCCCCCGAGCCAGGCCCAAGGCCCAAGTCCAGCCG	2343
Db	2335	GGCTCTGTGCACACTGCTGTGGCCCCCGAGCCAGGCCCAAGGCCCAAGTCCAGCCG	2394
Qy	2344	CAGACTTTGGAAAGCCCAAGCACTAGAGAGATGGGCCGTTGCCATGTGTGACGGAATC	2403
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Qy	2404	CGGGGGCTGGGGCTTTTGAATTGGCTTGGGGACTACTCGGCTCTCATCTCAGCTCCACG	2463
Db	2455	CGGGGGCTGGGGCTTTTGAATTGGCTTGGGGACTACTCGGCTCTCATCTCAGCTCCACG	2514
Qy	2464	GGAATCAGAGATGCGCGCCATCTGCTGAGGGTACTGTGCCCAATCTGTCCCAACCCA	2523
Db	2513	GGAATCAGAGATGCGCGCCATCTGCTGAGGGTACTGTGCCCAATCTGTCCCAACCCA	2574
Qy	2524	GCTGAGAGGCTGTCTCTCTTTCACACCCCTGGGGCCAG-CTCATTTGTGAGGGGCCAGG	2583
Db	2573	GCTGAGAGGCTGTCTCTCTTTCACACCCCTGGGGCCAGGCTCATTTGTGAGGGGCCAGG	2634
Qy	2583	CGTTGATCTTGAAGGCTCTGACATCTTAACTCTGTGCTGCTGCTGGGACAGAAATG	2643
Db	2633	CGTTGATCTTGAAGGCTCTGACATCTTAACTCTGTGCTGCTGCTGGGACAGAAATG	2694
Qy	2643	TGGCTCAGATGCTCTGTCTCTGTGGTGCACCTCGAAGGGACACTGTGATCTCTGTCAAT	2703
Db	2693	TGGCTCAGATGCTCTGTCTCTGTGGTGCACCTCGAAGGGACACTGTGATCTCTGTCAAT	2754
Qy	2703	TTTAACTCAGGTGACCCAGAGGGAGATGGGGCCCAAGGACAGACTTCAAGGGCCAGAGCC	2763
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Qy	2763	CTGACGAGAGAGAGGCCCTTTGCCAGAGACACAGACAGCTGGCTTAACTCTGAGGCC	2823
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ACCESSION AX358880  
VERSION AX358880.1 GI:18675341  
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SOURCE  
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REFERENCE  
AUTHORS 1  
Baker, K.P., Desnoyers, L., Gerlitsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
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QY 64 AACCTCACCCTCCCGGGATTCAGATTCATGACCTCCGAGAGTGGAGATT 123  
DB 115 AACCTCACCCTCCCGGGATTCAGATTCATGACCTCCGAGAGTGGAGATT 174  
QY 124 ACAGGTGTGACTTCCAGAGTACTCCGTGAGAGAAATGACTCCCGAGTGGCTG 183  
DB 175 ACAGGTGTGACTTCCAGAGTACTCCGTGAGAGAAATGACTCCCGAGTGGCTG 234  
QY 184 CAGACGACACTGTTCTGTGAGTCTGCTTCTGTGCTCAAGAGTGGAGAGG 243  
DB 235 CAGACGACACTGTTCTGTGAGTCTGCTTCTGTGCTCAAGAGTGGAGAGG 294  
QY 244 CACAGGAGAGACTTGTGCTCTGCAAGCAGAGAGACAGACAGAGAGAGCTTCAC 303  
DB 295 CACAGGAGAGACTTGTGCTCTGCAAGCAGAGAGAGACAGACAGAGAGAGCTTCAC 354  
QY 304 TACAAACCCACACACAGCTGCGCATCTCATGAGAACTCCGAGAGGCTTCACAGTC 363  
DB 355 TACAAACCCACACACAGCTGCGCATCTCATGAGAACTCCGAGAGGCTTCACAGTC 414  
QY 364 CAGTCCCTTCTCTGAGGAGCCACCTGCTTCCGATCTTCCCTGAGCCCGAGGGGCTC 423  
DB 415 CAGTCCCTTCTCTGAGGAGCCACCTGCTTCCGATCTTCCCTGAGCCCGAGGGGCTC 474  
QY 424 TACCACTTCTGCTCTACTGAAACCGACATGCTGGAAGATTACTTCTTATGGAAG 483  
DB 475 TACCACTTCTGCTCTACTGAAACCGACATGCTGGAAGATTACTTCTTATGGAAG 534  
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QY 664 GCCGCTCACAATGCTCTGAGTGAAGTGTGCAAGTCTCAAAAGGAACTCAGTGTCAAGC 723  
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DB 1255 TTCTGAGTGAAG 1314  
QY 1264 ACCGTGAG 1323  
DB 1315 ACCGTGAG 1374  
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DB 1375 CTGATGATCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1434  
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DB 1435 TACGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494  
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DB 1495 TCCAGAGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1554  
QY 1504 AACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563  
DB 1555 AACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1614  
QY 1564 CTGACAGAGCTCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1623  
DB 1615 CTGACAGAGCTCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1674  
QY 1624 ACCGTCTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1683  
DB 1675 ACCGTCTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1734  
QY 1684 TTGAGCACTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743



Db	655	AAACATCAGCCCTCCCAAGTCCGCCAGCTTCACTTCTTCCACAGTCTTCCCCACAG	714
Qy	664	GCOCCTCAACATAGCCTCGGTGGAATGTGCGAGCTCAAAAGGACCTCGAGTCTCAGC	723
Db	715	GCOCGTCAACATAGCCTCGGTGGAATGTGCGAGCTCAAAAGGACCTCGAGTCTCAGC	774
Qy	724	CAGTTCCTGAAGCATCCCCAGAAAGCCTCAAGAGAGCCCTCGGTGCCCCCGCAGCAG	783
Db	775	CAGTTCCTGAAGCATCCCCAGAAAGCCTCAAGAGAGCCCTCGGTGCCCCCGCAGCAG	834
Qy	784	CAGTTGCAGAGCCCTGAGTCGAAACTGACCTCTGTGAAATTCAATGGGGGACATGATGTCC	843
Db	835	CAGTTGCAGAGCCCTGAGTCGAAACTGACCTCTGTGAAATTCAATGGGGGACATGATGTCC	894
Qy	844	TTCCAGAGAGACCCGAGTCAATGCCACGGTATGAAAGCTCCAGCCCAAGCCCGCTTCAG	903
Db	895	TTCCAGAGAGACCCGAGTCAATGCCACGGTATGAAAGCTCCAGCCCAAGCCCGCTTCAG	954
Qy	904	GACCTGCACATCCACTCCCGCAGAGAGAGAGAGAGAGATCATGAGTACTTCGGTG	963
Db	955	GACCTGCACATCCACTCCCGCAGAGAGAGAGAGAGAGATCATGAGTACTTCGGTG	1014
Qy	964	CTGCTGCTCGAACACTTTTCAGAGAGCGAAAGCCGAGCCGGAGGAGCTGAGAGAGA	1023
Db	1015	CTGCTGCTCGAACACTTTTCAGAGAGCGAAAGCCGAGCCGGAGGAGCTGAGAGAGA	1074
Qy	1024	CTCTCTCTGTGTGAACTTTCAGAGAGCAGCCCTGTTCAGAGACAAATTCAGCAGATGC	1083
Db	1075	CTCTCTCTGTGTGAACTTTCAGAGAGCAGCCCTGTTCAGAGACAAATTCAGCAGATGC	1134
Qy	1084	CTGGGTGAGAAAGTCTTGGGAGATTGTGATACAGAACCAAGATAGCCAACTTCACGGAG	1143
Db	1135	CTGGGTGAGAAAGTCTTGGGAGATTGTGATACAGAACCAAGATAGCCAACTTCACGGAG	1194
Qy	1144	CCCGTGTGTCTCATCTTTCAGAGACCAAGTCAAGCCCGAATGTGATCTGTGTC	1203
Db	1195	CCCGTGTGTCTCATCTTTCAGAGACCAAGTCAAGCCCGAATGTGATCTGTGTC	1254
Qy	1204	TTCTGGGTTGAAGACCCCAATTTGAGACAGCCCGGGGCAATTGAGACAGTGGGTGTGAG	1263
Db	1255	TTCTGGGTTGAAGACCCCAATTTGAGACAGCCCGGGGCAATTGAGACAGTGGGTGTGAG	1314
Qy	1264	ACCGTCAGAGAGAAACCAACATCTGTCTTGTGCAACCACTTGACCTTATTTGACGTG	1323
Db	1315	ACCGTCAGAGAGAAACCAACATCTGTCTTGTGCAACCACTTGACCTTATTTGACGTG	1374
Qy	1324	CTGATGTGTCTCTCGGTGGAAGTGTGAGCCCGGTGCAAGCACTACGTGAGCTCTCTCC	1383
Db	1375	CTGATGTGTCTCTCGGTGGAAGTGTGAGCCCGGTGCAAGCACTACGTGAGCTCTCTCC	1434
Qy	1384	TACGTGGGCTGTGTGTGTCTGTGCTCTGTGCACTGTGTACACATTTGCCGCTTACCTCTGC	1443
Db	1435	TACGTGGGCTGTGTGTGTGTCTGTGCTCTGTGCACTGTGTACACATTTGCCGCTTACCTCTGC	1494
Qy	1444	TTCAGAGGTGCCCCCTGTGCGTGTGAGAGAGAACTTCGGGACTTACCACTAAAGTGCACATG	1503
Db	1495	TTCAGAGGTGCCCCCTGTGCGTGTGAGAGAGAACTTCGGGACTTACCACTAAAGTGCACATG	1554
Qy	1504	AACTGTGCTGAGCGGTCTTCTCTGTGTGACACAGACCTTCTGCTCAGAGAGCCCGGTGACC	1563
Db	1555	AACTGTGCTGAGCGGTCTTCTCTGTGTGACACAGACCTTCTGCTCAGAGAGCCCGGTGACC	1614
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Qy	1624	ACCTGCTTCTCTGTGATGGGCTCTCAGAGGGGTACAACTTACCGACTGTGTGTGAGGCTC	1683
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[illegible]





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Db	2335	GGCGCTCGTGCACACTGCTGTGTGGCGCCCGAGCGAGGCCCAAGGCCCAAGCGCATGCAGCG	2394
QY	2344	CAGACTTTGGAAAGCCCAAGCAACATGGAGAGATGGGCGCTTGGCATGTGTGAAGAGGAGTGC	2403
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SOURCE					
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REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E., Geo, W. Q., Gerritsen, M. E., Goddard, A., Godowski, P. J., Gunney, A. L., Sherwood, S., Smith, V., Stewart, T. A., Tuma, D., Watanabe, C. K., Wood, W. L. and Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding same				
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QY	124 ACAGGTGTGATCTTCCAGAGTGAATCCGTGGAGGAAATGATCTCCCAAGTCGTGCTG	183			
DB	175 ACAGGTGTGATCTTCCAGAGTGAATCCGTGGAGGAAATGATCTCCCAAGTCGTGCTG	234			
QY	184 CAGAGCAGCTGTCTCTGCTAGTCTGCTCTTCTGTCTCAAGGTGCCAAGGCAAGGGGC	243			
DB	235 CAGAGCAGCTGTCTCTGCTAGTCTGCTCTTCTGTCTCAAGGTGCCAAGGCAAGGGGC	294			
QY	244 CACAGGGGAAAGCTTTGGCTTGTGACAGGCGGAAACAGACACACAGGAGAGCTTCCAC	303			
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## RESULT 13

AX490984 3819 bp DNA linear PAT 16-AUG-2002  
LOCUS AX490984  
DEFINITION Sequence 91 from Patent WO200690.  
ACCESSION AX490984  
VERSION AX490984.1 GI:22323829

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gertlisen, M.E., Goddard, A.,  
Godowski, P., Gurey, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Poon, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 020690-A 91 03-JAN-2002;  
Genentech, Inc. (US)

FEATURES  
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/mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 98.6%; Score 2783.4; DB 6; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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QY 244 CACAGGAGAGACTTTCGCTTGTGACGCGAGGAGAACAGACACACAGAGAGCTTCAC 303  
Db 295 CACAGGAGAGACTTTCGCTTGTGACGCGAGGAGAACAGACACACAGAGAGCTTCAC 354  
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Db 415 CAGCAGCCTTTCCTGACAGCCACCTGCTTCCGATCTTCCCTGACCCAGAGGAGCTC 474  
QY 424 TACCACTTTCGCTTCTATCTGAACTGCAATGCTGGAGATTCATCTTCTATATGGCAAG 483  
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QY 1564 CTGAGAGGCTCTGAGGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623

Db	1615	CTGACAGGCTCTAAGGCTGGCTGCGCCGAGCGAGTGCATCTTCTGTGCATCTTCCCTGCTC	1674
Qy	1624	ACCTGACCTTTCTGTGATGAGGCTCTGAGGGGTACAACTCTACCGACTGTGTGAGGTC	1683
Db	1675	ACCTGCGCTTTCCGTGATGAGGCTCTGAGGGGTACAACTCTACCGACTGTGTGAGGTC	1734
Qy	1684	TTTGGCACTTAATGTCCCTGGCTACTACTCAACTGAGGCCATGGGCGTGGGGCTTCCCC	1743
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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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## ORIGIN

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Query Match 98.4%; Score 2778.2; DB 9; Length 3702;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2806; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

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QY 846 CGAGAGAGACCGATCAACGCGACGATATGAAAGCTTCAGGCCACAGCGGCTTCAGGA 905  
DB 842 CGAGAGAGACCGATCAACGCGACGATATGAAAGCTTCAGGCCACAGCGGCTTCAGGA 901  
QY 906 CTTGCAATCACTTCCGCGAGAGAGAGAGACAGGCGAGATCATGAGTACTCGGTCT 965  
DB 902 CTTGCAATCACTTCCGCGAGAGAGAGAGACAGGCGAGATCATGAGTACTCGGTCT 961

QY 966 GCTGCTCCGACACACTCTTCCAGAGAGCGAAAGGCGGAGGCGGTGAGAGACT 1025  
DB 962 GCTGCTCCGACACACTCTTCCAGAGAGCGAAAGGCGGAGGCGGTGAGAGACT 1021  
QY 1026 CTTCTGTGAGACTTTCAGACAGCCGACCTGTTTCAGAGACAGAAATTCAGCCAGTCT 1085  
DB 1022 CTTCTGTGAGACTTTCAGACAGCCGACCTGTTTCAGAGACAGAAATTCAGCCAGTCT 1081  
QY 1086 GGGTGAAGAGCTTGGGGATTTGTGTACAGAAACCAAGATAGCCACTCAGCGAGCC 1145  
DB 1082 GGGTGAAGAGCTTGGGGATTTGTGTACAGAAACCAAGATAGCCACTCAGCGAGCC 1141  
QY 1146 CGTGTGCTCACTTTCAGAGACCACTACAGCCGAGAAATGTGACTCTGCAATGTGTT 1205  
DB 1142 CGTGTGCTCACTTTCAGAGACCACTACAGCCGAGAAATGTGACTCTGCAATGTGTT 1201  
QY 1206 CTTGGTTGAAGACCCCACTTGAAGACCCGCGGCAATTGAAGAGTCTGGGTGTGAGAC 1265  
DB 1202 CTTGGTTGAAGACCCCACTTGAAGACCCGCGGCAATTGAAGAGTCTGGGTGTGAGAC 1261  
QY 1266 CGTGAGAGAGAAACCAACATCTCTGTTCTGACACATTCATCTTGAAGAGTCT 1325  
DB 1262 CGTGAGAGAGAAACCAACATCTCTGTTCTGACACATTCATCTTGAAGAGTCT 1321  
QY 1326 GATGTCTCTCGGTGAGAGGTGAGACGCGGTGACACACATCTGAGGCTCTCTCTA 1385  
DB 1322 GATGTCTCTCGGTGAGAGGTGAGACGCGGTGACACACATCTGAGGCTCTCTCTA 1381  
QY 1386 CGTGGGCTGTGTGCTCTCTGCGCTGAGCTTGTGACATTCGCGCTACCTCTGCTC 1445  
DB 1382 CGTGGGCTGTGTGCTCTCTGCGCTGAGCTTGTGACATTCGCGCTACCTCTGCTC 1441  
QY 1446 CAGGGTCCCTGCGCTGTCAGAGAGAAACCTCGGAGATCAACATCAAGGTCACATGAA 1505  
DB 1442 CAGGGTCCCTGCGCTGTCAGAGAGAAACCTCGGAGATCAACATCAAGGTCACATGAA 1501  
QY 1506 CTTGCTGTGGCGCTCTTCTCTGTCGACACAGGCTTCTGTCAGGAGCGGTGGCCCT 1565  
DB 1502 CTTGCTGTGGCGCTCTTCTCTGTCGACACAGGCTTCTGTCAGGAGCGGTGGCCCT 1561  
QY 1566 GACAGGCTCTGAGGCTGTGCGAGGACGATGTCATCTTCTGACATTCGCGCTCAC 1625  
DB 1562 GACAGGCTCTGAGGCTGTGCGAGGACGATGTCATCTTCTGACATTCGCGCTCAC 1621  
QY 1626 CTTGCTTTCCTGAGATGGGCTCGAGGGGTACAACTTCAAGGCTGCTGTGAGTCTT 1685  
DB 1622 CTTGCTTTCCTGAGATGGGCTCGAGGGGTACAACTTCAAGGCTGCTGTGAGTCTT 1681  
QY 1686 TGGACCTATGTCCTGAGCTACTTCAAGCTGAGCGCAATGGGCTTGGGCTTCCCAT 1745  
DB 1682 TGGACCTATGTCCTGAGCTACTTCAAGCTGAGCGCAATGGGCTTGGGCTTCCCAT 1741  
QY 1746 CTTTCTGTGAGCGCTGTGCGCTGCTGTGAGATGTGAGCAACATAGGCGGCACTTGGG 1805  
DB 1742 CTTTCTGTGAGCGCTGTGCGCTGCTGTGAGATGTGAGCAACATAGGCGGCACTTGGG 1801  
QY 1806 TGTGCATTAAGACTCAGAGGCGCTCATCTTCACTTGCATGTGAGATCCGCGACTCCCT 1865  
DB 1802 TGTGCATTAAGACTCAGAGGCGCTCATCTTCACTTGCATGTGAGATCCGCGACTCCCT 1861  
QY 1866 GGTGAGCTATCATCAACCACTTGGGCTTTCAGGCTGTGTTCTGTTCACAATGGCCAT 1925  
DB 1862 GGTGAGCTATCATCAACCACTTGGGCTTTCAGGCTGTGTTCTGTTCACAATGGCCAT 1921  
QY 1926 GCTAGCCACATATGATGTGAGATTCGCGGCTGCGCCCAACCCAAAGTGTGTACA 1985  
DB 1922 GCTAGCCACATATGATGTGAGATTCGCGGCTGCGCCCAACCCAAAGTGTGTACA 1981  
QY 1986 TGTGTGACACTGTGAGGCTCAGGCTGTGCTTGTGAGCTTGTGAGCTTGTGATTTCTT 2045  
DB 1982 TGTGTGACACTGTGAGGCTCAGGCTGTGCTTGTGAGCTTGTGAGCTTGTGATTTCTT 2041







identified by the method of the invention, is useful as an appetite control agent for controlling appetite in an individual. The dominant negative mutant of GPR56 is useful for evaluating the role of GPR56 in the control of appetite. A transgenic non-human animal containing the GPR56 gene is useful for evaluating the effects of test compounds in appetite control and obesity. The agonists or antagonists of GPR56 are useful as appetite control agents for controlling obesity. AON is also useful as an appetite control agent. This polynucleotide sequence CC represents the cDNA of the human G protein-coupled receptor, GPR56, of the invention

XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

Query Match 100.0%; Score 2822; DB 6; Length 2822;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACAGAGGCTCTCGCTCTGTCAACAGGCTGGAGTGCAGTGTGATCTTGGCTCAT 60  
DB 1 CGGACAGAGGCTCTCGCTCTGTCAACAGGCTGGAGTGCAGTGTGATCTTGGCTCAT 60  
QY 61 CGTAACTCCACCTCCGGGTTCAAGTATTCATGCTCAGGCTCCGAGTACTGG 120  
DB 61 CGTAACTCCACCTCCGGGTTCAAGTATTCATGCTCAGGCTCCGAGTACTGG 120  
QY 121 ATTACAGGTGTGATCTTCCAAAGTGAATCCGTGAGGAAATGACTCCCAAGTCTG 180  
DB 121 ATTACAGGTGTGATCTTCCAAAGTGAATCCGTGAGGAAATGACTCCCAAGTCTG 180  
QY 181 CTGCAAGACGACCTGTTCTCTGTGAGTGTGCTCTTCTGCTCCAAAGTGTCCAGGAG 240  
DB 181 CTGCAAGACGACCTGTTCTCTGTGAGTGTGCTCTTCTGCTCCAAAGTGTCCAGGAG 240  
QY 241 GGCACACAGGGAAGCTTTCGCTTCTGACGACGAGGAGACAGACACAGAGAGGCTC 300  
DB 241 GGCACACAGGGAAGCTTTCGCTTCTGACGACGAGGAGACAGACACAGAGAGGCTC 300  
QY 301 CACTCAAAACCCACACAGACCTGCGATCTCATGAGAACTCCGAAGAGGCTTCA 360  
DB 301 CACTCAAAACCCACACAGACCTGCGATCTCATGAGAACTCCGAAGAGGCTTCA 360  
QY 361 GTCCATGCCCCCTTCCCTGAGGCCACCGCTTCCGATCTTCCCTGACCCAGGAGC 420  
DB 361 GTCCATGCCCCCTTCCCTGAGGCCACCGCTTCCGATCTTCCCTGACCCAGGAGC 420  
QY 421 CTCTACCACTTCTGCTCTACTGGAACGACATGCTGGAGATTACATCTTCTATG 480  
DB 421 CTCTACCACTTCTGCTCTACTGGAACGACATGCTGGAGATTACATCTTCTATG 480  
QY 481 AAGGTGACTTCTTGTGAGTGAAGAAAGCTCTAGCTCTGCTTCCAGACACAGAG 540  
DB 481 AAGGTGACTTCTTGTGAGTGAAGAAAGCTCTAGCTCTGCTTCCAGACACAGAG 540  
QY 541 GAGAGCTGGCTGAGGAGCCCCCGCTGTAGCACTTCTGACCTCCGTGTGAGGCT 600  
DB 541 GAGAGCTGGCTGAGGAGCCCCCGCTGTAGCACTTCTGACCTCCGTGTGAGGCT 600  
QY 601 CAGAACATCAGCTGCGCAGTGCAGGCTTCACTTCTCTTCCAGAGTCTCCAC 660  
DB 601 CAGAACATCAGCTGCGCAGTGCAGGCTTCACTTCTCTTCCAGAGTCTCCAC 660  
QY 661 ACGGCGCTCAATATGCTCGGTGAGCATGTGCGAGCTCAAAAGGAACTTCAAGTGT 720  
DB 661 ACGGCGCTCAATATGCTCGGTGAGCATGTGCGAGCTCAAAAGGAACTTCAAGTGT 720  
QY 721 AGCCAGTTCTGGAAGATCCCAAGAGGCTCAAGAGGCTTGGGCTGCCCGGCAAG 780  
DB 721 AGCCAGTTCTGGAAGATCCCAAGAGGCTCAAGAGGCTTGGGCTGCCCGGCAAG 780  
QY 781 CAGCAGTTGCAAGAGCTGAGTGCAGAACTGACCTTGTGAGATTCAATGGGGAATG 840  
DB 781 CAGCAGTTGCAAGAGCTGAGTGCAGAACTGACCTTGTGAGATTCAATGGGGAATG 840

QY 841 TCCTTGAGAGAGACCGGATCAACGCCACGATGTGAAGCTCCAGCCACAGCCGCTC 900  
DB 841 TCCTTGAGAGAGACCGGATCAACGCCACGATGTGAAGCTCCAGCCACAGCCGCTC 900  
QY 901 CAGACCTCAATCACTCCCGGAGAGAGAGACAGAGGAGATCATGAGTACTG 960  
DB 901 CAGACCTCAATCACTCCCGGAGAGAGAGACAGAGGAGATCATGAGTACTG 960  
QY 961 GTGCTGCTCTGAAACACTCTTCCAGAGAGAGAAAGCCGAGAGCGGAGGCTGAGAG 1020  
DB 961 GTGCTGCTCTGAAACACTCTTCCAGAGAGAGAAAGCCGAGAGCGGAGGCTGAGAG 1020  
QY 1021 AGACTCTCTGTGATCACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
DB 1021 AGACTCTCTGTGATCACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
QY 1081 GTCTGAGTGAAGAGCTTGGGAGATTGTGATCAAGAACCAAGATGACTTGCATAT 1140  
DB 1081 GTCTGAGTGAAGAGCTTGGGAGATTGTGATCAAGAACCAAGATGACTTGCATAT 1140  
QY 1141 GAGCCGCTGAGTCACTTCCAGACACAGCTACAGCCGAGAAATGTGACTTGCATAT 1200  
DB 1141 GAGCCGCTGAGTCACTTCCAGACACAGCTACAGCCGAGAAATGTGACTTGCATAT 1200  
QY 1201 GTGTTCTGGTGAAGACCCCATTTGAGAGAGCCGAGGCAATGAGAGTGTG 1260  
DB 1201 GTGTTCTGGTGAAGACCCCATTTGAGAGAGCCGAGGCAATGAGAGTGTG 1260  
QY 1261 GAGACGCTGAGAGAGAAACCAACATCTGCTTGTGACACCACTTGAACCTTGA 1320  
DB 1261 GAGACGCTGAGAGAGAAACCAACATCTGCTTGTGACACCACTTGAACCTTGA 1320  
QY 1321 GTGCTGATGCTCTCTCGGTGAGAGTGAAGCCGCTGACAGAGACCTGAGCCTC 1380  
DB 1321 GTGCTGATGCTCTCTCGGTGAGAGTGAAGCCGCTGACAGAGACCTGAGCCTC 1380  
QY 1381 TCCATGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
DB 1381 TCCATGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
QY 1441 TGTCTCAAGAGTGCCTTCCGCTGAGAGAGAACTTGGAGCTACACATCAAGTGT 1500  
DB 1441 TGTCTCAAGAGTGCCTTCCGCTGAGAGAGAACTTGGAGCTACACATCAAGTGT 1500  
QY 1501 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 1501 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
QY 1561 GCCCTGACAGCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
DB 1561 GCCCTGACAGCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
QY 1621 CTGACCTGCTTCTGAGTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
DB 1621 CTGACCTGCTTCTGAGTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
QY 1681 GTCTTGTGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
DB 1681 GTCTTGTGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 CCAATCTTCTGAGTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
DB 1741 CCAATCTTCTGAGTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 TTGCTGCTGATGAGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
DB 1801 TTGCTGCTGATGAGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 1861 TTGCTGCTGATGAGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
DB 1861 TTGCTGCTGATGAGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
QY 1921 GCAATGCTAGCACATGATGTGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
DB 1921 GCAATGCTAGCACATGATGTGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCT 1980

Db	1921	GGCATGTAGCCACCAAGGTGGTGCAGATCTTGGCTGGGCCCCACACCCAAAGTGG	1980
Qy	1981	TCACATGTGTGACACACTGTGGGCTCAAGCTGGTCTTGGGCTGTGGGCTTGATC	2040
Db	1981	TGACATGTGTGACACTGTGGGCTCAAGCTGGTCTTGGGCTGTGGGCTTGATC	2040
Qy	2041	TTCTTCTCTTGTGCTTGGGACCTTCAAGCTTGTGTGCTCTAACCTTTTCAAGCATC	2100
Db	2041	TTCTTCTCTTGTGCTTGGGACCTTCAAGCTTGTGTGCTCTAACCTTTTCAAGCATC	2100
Qy	2101	ACCTCTTCAAGAGGCTTCTCATCTTCATCTGTACTGTGTCACTGGGGCTGAGGCCGG	2160
Db	2101	ACCTCTTCAAGAGGCTTCTCATCTTCATCTGTACTGTGTCACTGGGGCTGAGGCCGG	2160
Qy	2161	GGTGGCCCTCCCTCTTGAAGAGCACTGAGCTGGGCTCCCACTCAAGCTGGGGC	2220
Db	2161	GGTGGCCCTCCCTCTTGAAGAGCACTGAGCTGGGCTCCCACTCAAGCTGGGGC	2220
Qy	2221	AGCACCTGTCCAGGCGCATCTTGGGCTCCAGGCCACTTACCCTATGTATGAAGACAGA	2280
Db	2221	AGCACCTGTCCAGGCGCATCTTGGGCTCCAGGCCACTTACCCTATGTATGAAGACAGA	2280
Qy	2281	TGCGGCTCTGTGCGACACTGCTGTGGCCCCCGAGCGGCCCAAGCCCAAGCGATCAG	2340
Db	2281	TGCGGCTCTGTGCGACACTGCTGTGGCCCCCGAGCGGCCCAAGCCCAAGCGATCAG	2340
Qy	2341	CCGAGACTTTGGAAAGCCCAACCATGTAGAGAGTGGGCCGTTGGCATGTGGAGAGGA	2400
Db	2341	CCGAGACTTTGGAAAGCCCAACCATGTAGAGAGTGGGCCGTTGGCATGTGGAGAGGA	2400
Qy	2401	CTCCCGGAGCTGGGGCTTTTGAATTGGCTTTGGGAGCTACTCGGCTCTCACTCAGCTCC	2460
Db	2401	CTCCCGGAGCTGGGGCTTTTGAATTGGCTTTGGGAGCTACTCGGCTCTCACTCAGCTCC	2460
Qy	2461	ACGGGACTCAGAAATGGCGCGCCCATGTGCTAGAGTACTGTCCCCCATCTGTGCCAAC	2520
Db	2461	ACGGGACTCAGAAATGGCGCGCCCATGTGCTAGAGTACTGTCCCCCATCTGTGCCAAC	2520
Qy	2521	CCAGCTGAGGACTGTGCTCTCTTCAACACCCTTGGGCCCAAGCTCAATTGCTGGGGGCA	2580
Db	2521	CCAGCTGAGGACTGTGCTCTCTTCAACACCCTTGGGCCCAAGCTCAATTGCTGGGGGCA	2580
Qy	2581	GGCCTTGATCTTGAAGGCTGTGGCAATCTTAACTGTGCCCCCTGTGGGACAGAA	2640
Db	2581	GGCCTTGATCTTGAAGGCTGTGGCAATCTTAACTGTGCCCCCTGTGGGACAGAA	2640
Qy	2641	TGTGGCTCCAAATGCTGTGCTCTGTGCTGTGAGTCAACCTTGAAGGCACTTGCATCTCTGCA	2700
Db	2641	TGTGGCTCCAAATGCTGTGCTCTGTGCTGTGAGTCAACCTTGAAGGCACTTGCATCTCTGCA	2700
Qy	2701	TTTTAACCTCAGTGGCAACCAAGGCGAATGGGGCCAGGGCAGACTTCAAGGGCAGAG	2760
Db	2701	TTTTAACCTCAGTGGCAACCAAGGCGAATGGGGCCAGGGCAGACTTCAAGGGCAGAG	2760
Qy	2761	CCCTTGGCGAGAGAGGCCCTTGGCAAGAGACAGACAGAGCTGGCTTACTCTGAGCC	2820
Db	2761	CCCTTGGCGAGAGAGGCCCTTGGCAAGAGACAGACAGAGCTGGCTTACTCTGAGCC	2820
Qy	2821	CG 2822	
Db	2821	CG 2822	
RESULT 2			
ABA05329 standard; DNA; 2822 BP.			
ABA05329;			
27-FEB-2002 (first entry)			
Human GPR56 encoding DNA.			

XX	Human; GPR22; anorectic; appetite control agent; GPR; gene;
XX	G protein-coupled receptor; orphan receptor; antisense gene therapy;
KM	mouse; GPR56; ds.
XX	
OS	Homo sapiens.
XX	
XX	MO200183550-A2.
FN	
XX	08-NOV-2001.
PD	
XX	30-APR-2001; 2001MO-GB001874.
PF	
XX	03-MAY-2000; 2000US-020141BP.
PR	
PA	(ASTR ) ASTRAZENECA AB.
XX	(ASTR ) ASTRAZENECA UK LTD.
P1	Brennard JC, Hart KA;
DR	WPI; 2002-066519/09.
PT	
PT	Identifying appetite control agent for controlling obesity, comprises
PT	screening agonists or antagonists of G protein-coupled receptor, GPR22,
PT	and using them as test compounds in appetite control test procedures.
XX	
PS	Claim 6; Page 18-19; 21pp; English.
CC	
CC	The invention relates to identifying an anorectic appetite control agent,
CC	comprising screening for agonists and/or antagonists of G protein-coupled
CC	receptor GPR22 (an orphan receptor), using one or more agonists and/or
CC	antagonists so identified as test compounds in one or more appetite
CC	control procedures and selecting an active compound for use as an
CC	appetite control agent. An antisense oligonucleotide to the GPR22 gene is
CC	also useful for controlling obesity using antisense gene therapy. Note:
CC	The GPR22 encoding cDNA sequence (AB05328) and encoded protein
CC	(AA047903) are disclosed, however two DNA sequences described as human
CC	(AB05329) and mouse (AB05328) GPR56 are given in the sequence listing
CC	, but are not otherwise referred to in the specification
XX	
SQ	Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;
XX	
XX	Query Match 100.0%; Score 2822; DB 6; Length 2822;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

  

OY	1 CGCGACGAGGGCTTCGTCTGCACACAGGGCTGAGTGCAGTGATCTTGCTCAT	60
D8		
OY	1 CGCGACGAGGGCTTCGTCTGCACACAGGGCTGAGTGCAGTGATCTTGCTCAT	60
D8		
OY	61 CGTAACCTCACCCTCCCGGGTTCAAGTATTCTCATGTCCAGCTCCCGAAGTAGCTGG	120
D8	61 CGTAACCTCACCCTCCCGGGTTCAAGTATTCTCATGTCCAGCTCCCGAAGTAGCTGG	120
OY	121 ATTACAGGTGTGAATCTTCCAAGTGAATCTCCGTCCGAGAAGAAATGACTCCCAGTGCCTG	180
D8	121 ATTACAGGTGTGAATCTTCCAAGTGAATCTCCGTCCGAGAAGAAATGACTCCCAGTGCCTG	180
OY	181 CTGACAGACAATCTGTTCTGTGAGTCTGCTCTTCTGTGCCAAGTGTCCACGCGAAGS	240
D8	181 CTGACAGACAATCTGTTCTGTGAGTCTGCTCTTCTGTGCCAAGTGTCCACGCGAAGS	240
OY	241 GGCCACAGGGAAGACTTTTGCTTCTGCAGCCGACGGGAATCAACACACACAGAGAGAGCCCTC	300
D8	241 GGCCACAGGGAAGACTTTTGCTTCTGCAGCCGACGGGAATCAACACACACAGAGAGAGCCCTC	300
OY	301 CATTAACAACCAACACACAGACCGGAGCTCTCATGAGAACTCCGAAAGAGGCGCTCAC	360
D8	301 CATTAACAACCAACACACAGACCGGAGCTCTCATGAGAACTCCGAAAGAGGCGCTCAC	360
OY	361 GTTCATGCCCCCTTCCCTGAGCCACCCCTGCTCCCATTCCTTCCCTGACCCCAAGGGG	420
D8	361 GTTCATGCCCCCTTCCCTGAGCCACCCCTGCTCCCATTCCTTCCCTGACCCCAAGGGG	420

Oy	421	CTTACCACTTCTGCTCTTACTGGAACCGACATCTCTGGAGATTACATCTTCTCTATGTC	480
Db	421	CTTACCACTTCTGCTCTTACTGGAACCGACATCTCTGGAGATTACATCTTCTCTATGTC	480
Oy	481	AAAGGTGACTTCTTGCTGAGTGAAGAAAGCTCTTGACCTCTCTGCTTCCAGACACAGAG	540
Db	481	AAAGGTGACTTCTTGCTGAGTGAAGAAAGCTCTTGACCTCTCTGCTTCCAGACACAGAG	540
Oy	541	GAGAGCTGCTCAGAGGCCCGCTGTTAGCCACTTCTGTCACTTCTGAGTGGAGCCTT	600
Db	541	GAGAGCTGCTCAGAGGCCCGCTGTTAGCCACTTCTGAGTGGAGCCTT	600
Oy	601	CAGAAACATCAACCTGCCACAGTGGCCGACGCTTACCTTCTCTTCCACAGTCTCCCCAC	660
Db	601	CAGAAACATCAACCTGCCACAGTGGCCGACGCTTACCTTCTCTTCCACAGTCTCCCCAC	660
Oy	661	ACGGCCGCTCAAAATGCTCTGGTGAACATGTGCGAGCTCAAAAGGACCTTCAGCTGCTC	720
Db	661	ACGGCCGCTCAAAATGCTCTGGTGAACATGTGCGAGCTCAAAAGGACCTTCAGCTGCTC	720
Oy	721	AGCCAGTTCCTGAAGCATTCGCCAAGAGCCTTCAGAGAGCCTTGCGTCCCGCCAGC	780
Db	721	AGCCAGTTCCTGAAGCATTCGCCAAGAGCCTTCAGAGAGCCTTGCGTCCCGCCAGC	780
Oy	781	CAGCAGTTGCAGAGCTGAGATCGAAACTGACCTCTGTGAGATTCAATGGGGACATGCTG	840
Db	781	CAGCAGTTGCAGAGCTGAGATCGAAACTGACCTCTGTGAGATTCAATGGGGACATGCTG	840
Oy	841	TCTTTGAGAGAGACCGGATCAACGCCACGGTATGAAAGCTTCAGCCCAACGCCGCTC	900
Db	841	TCTTTGAGAGAGACCGGATCAACGCCACGGTATGAAAGCTTCAGCCCAACGCCGCTC	900
Oy	901	CAGGACCTGCACATCACTCCCGCAGAGAGAGAGACAGACGAGATCATGGAATACCG	960
Db	901	CAGGACCTGCACATCACTCCCGCAGAGAGAGAGACAGACGAGATCATGGAATACCG	960
Oy	961	GTGCTGCTGCTCGAACACTCTTCCAGAGAGCAAGAAAGCCGAGCCGGAGGCTGAGAG	1020
Db	961	GTGCTGCTGCTCGAACACTCTTCCAGAGAGCAAGAAAGCCGAGCCGGAGGCTGAGAG	1020
Oy	1021	AGACTCTCTCTGTGTGGAATTTCAAGAGCCACCTCTTCCAGAGCAAGAAATTCAGGCCA	1080
Db	1021	AGACTCTCTCTGTGTGGAATTTCAAGAGCCACCTCTTCCAGAGCAAGAAATTCAGGCCA	1080
Oy	1081	GTCTCTGAGTGAAGAGTCTTGAGGATTTGTGTACAGAACCAACAAATGAGCCATCAGC	1140
Db	1081	GTCTCTGAGTGAAGAGTCTTGAGGATTTGTGTACAGAACCAACAAATGAGCCATCAGC	1140
Oy	1141	GAGCCGTGTGTCTCACTTTCCAGACCAAGCTACAGCCGAGAAATGTGACTCTGCAATGT	1200
Db	1141	GAGCCGTGTGTCTCACTTTCCAGACCAAGCTACAGCCGAGAAATGTGACTCTGCAATGT	1200
Oy	1201	GTGTTCTGGGTTGAAGACCCCAATTTGAGACGCCGGGACATTTGAGAGTGTGGGTGT	1260
Db	1201	GTGTTCTGGGTTGAAGACCCCAATTTGAGACGCCGGGACATTTGAGAGTGTGGGTGT	1260
Oy	1261	GAGACCGTCAAGAGAGAAACCAACATCTGTCTTCTGCAACCACTTGACTTACTTTGCA	1320
Db	1261	GAGACCGTCAAGAGAGAAACCAACATCTGTCTTCTGCAACCACTTGACTTACTTTGCA	1320
Oy	1321	GTGCTGATGTGTTCTCTCGTGAAGTGAACGCCCGTGCACAAAGCACTACCTGAGCTCTC	1380
Db	1321	GTGCTGATGTGTTCTCTCGTGAAGTGAACGCCCGTGCACAAAGCACTACCTGAGCTCTC	1380
Oy	1381	TCTTCAAGTGGCTGTGTCTCTTCTGACCTTGACCTTGTCAACATTTGCGGCTCACTC	1440
Db	1381	TCTTCAAGTGGCTGTGTCTCTTCTGACCTTGTCAACATTTGCGGCTCACTC	1440
Oy	1441	TGCTTCAAGGTGCCCCCTGCGGTGCAGAGAGAAACCTCGGACATTAACAATCAAGGTGAC	1500
Db	1441	TGCTTCAAGGTGCCCCCTGCGGTGCAGAGAGAAACCTCGGACATTAACAATCAAGGTGAC	1500

Qy	1501	ATGAACCTGCTGTGGCCGCTCTTCTCTGTGGAACAAGAGCTTCTGTGACGACGCCGCGGAG	1560
Db	1501	ATGAACCTGCTGTGGCCGCTCTTCTCTGTGGAACAAGAGCTTCTGTGACGACGCCGCGGAG	1560
Qy	1561	GCCCTGACAGAGCTCTGAGGCTGGGCTGCGCAGGACGAGGCCATCTTCTGTGACTTCTCCCTG	1620
Db	1561	GCCCTGACAGAGCTCTGAGGCTGGGCTGCGCAGGACGAGGCCATCTTCTGTGACTTCTCCCTG	1620
Qy	1621	CTCACTGCTCTTCTGTGATGGGCTTCGAGGGGTACAACTCTTACCGACTTCGTGTGGAG	1680
Db	1621	CTCACTGCTCTTCTGTGATGGGCTTCGAGGGGTACAACTCTTACCGACTTCGTGTGGAG	1680
Qy	1661	GTCCTTGGGACCTATATGTCCTGGCTACCTACCTAAGCTAGGCGCAATGGGCTGGGGCTTC	1740
Db	1661	GTCCTTGGGACCTATATGTCCTGGCTACCTACCTAAGCTAGGCGCAATGGGCTGGGGCTTC	1740
Qy	1741	CCCATCTTCTGTGTGACGCTGTGTGGCCCTGTGGATGTGGACAATATGAGCCCATATC	1800
Db	1741	CCCATCTTCTGTGTGACGCTGTGTGGCCCTGTGGATGTGGACAATATGAGCCCATATC	1800
Qy	1801	TTGGCTGTGCAATAGGATCTCCAGAGGGGTATATACCTTCCATATGTGCTGAATCCGGAGAC	1860
Db	1801	TTGGCTGTGCAATAGGATCTCCAGAGGGGTATATACCTTCCATATGTGCTGAATCCGGAGAC	1860
Qy	1861	TCCCTGTGACGCTACATACCAACTGGGCTCTTCAAGCTGTGTTCGTTCAACATG	1920
Db	1861	TCCCTGTGACGCTACATACCAACTGGGCTCTTCAAGCTGTGTTCGTTCAACATG	1920
Qy	1921	GCCATGCTAGCAACCATGTGTGTGACATCTCTGCGCTGGCGCCCAACCCAAAGTGG	1980
Db	1921	GCCATGCTAGCAACCATGTGTGTGACATCTCTGCGCTGGCGCCCAACCCAAAGTGG	1980
Qy	1961	TCACATGTGCGACACTGTGTGGGCTCAGCTGGTCTTGTGGCTGTGGCTTGGGCTTGATC	2040
Db	1961	TCACATGTGCGACACTGTGTGGGCTCAGCTGGTCTTGTGGCTGTGGCTTGGGCTTGATC	2040
Qy	2041	TTCTTCTCTCTTGTGCTTGTGGACCTTCCAGCTTGTGCTCTTACCTTTTCAAGATATC	2100
Db	2041	TTCTTCTCTCTTGTGCTTGTGGACCTTCCAGCTTGTGCTCTTACCTTTTCAAGATATC	2100
Qy	2101	AACCTCTTCCAGGCTTCTCATCTTTCATGTGTGACTGTGTCAATGCGGCTGACAGGCTCGG	2160
Db	2101	AACCTCTTCCAGGCTTCTCATCTTTCATGTGTGACTGTGTCAATGCGGCTGACAGGCTCGG	2160
Qy	2161	GGTGGCCCCCTCCCTCTGTGAAGAGCACTCAGACTGTGCGCAAGCTCCCTCATGCTGGGCT	2220
Db	2161	GGTGGCCCCCTCCCTCTGTGAAGAGCACTCAGACTGTGCGCAAGCTCCCTCATGCTGGGCT	2220
Qy	2221	AGCACTGTGTCAAGCCGCACTTAAAGGCTCCAGGCCCACTGSCCATATGTATGAAGACAGAA	2280
Db	2221	AGCACTGTGTCAAGCCGCACTTAAAGGCTCCAGGCCCACTGSCCATATGTATGAAGACAGAA	2280
Qy	2281	TGCGGCTCTGTGTGCACTGTGCTGTGGCCCCGAGCCAGGCCAAGGCCCAAGCTCAG	2340
Db	2281	TGCGGCTCTGTGTGCACTGTGCTGTGGCCCCGAGCCAAGGCCAAGGCCCAAGCTCAG	2340
Qy	2341	CCGCAACTTTGGAAAGCCCAACGACATGAGAGATATGGGCGCTTTGGCAATGTGTGAAGAA	2400
Db	2341	CCGCAACTTTGGAAAGCCCAACGACATGAGAGATATGGGCGCTTTGGCAATGTGTGAAGAA	2400
Qy	2401	CTTCCCGGGGCTGGGGCTTTTGAATTGGGCTTGGGGAATTAAGCTGGCTCTCACTCACTCC	2460
Db	2401	CTTCCCGGGGCTGGGGCTTTTGAATTGGGCTTGGGGAATTAAGCTGGCTCTCACTCACTCC	2460
Qy	2461	ACGGGACTTGAAGTGGCGCGCATGTGCTTAAAGGTACTGTCCCACTATGTGCCAAC	2520
Db	2461	ACGGGACTTGAAGTGGCGCGCATGTGCTTAAAGGTACTGTCCCACTATGTGCCAAC	2520
Qy	2521	CCAGCTGAGAGGCTGTGTCTCTCTTCAACCCCTGGGCCAGGCTCAATGTCTGGGGGGCA	2580
Db	2521	CCAGCTGAGAGGCTGTGTCTCTCTTCAACCCCTGGGCCAGGCTCAATGTCTGGGGGGCA	2580
Qy	2581	GGCCTTGAATCTTGAAGGCTGTGGCAATCTTAAATCTGTGCCCCCTGTGGGACAGAAA	2640

DB 2581 GGCCTTGATCTTGAGGGTGTGGACATCTTATCTGTGCCCCCTGCGGAGCAGAA 2640  
 QY 2641 TGTGGCTCCAGTGTCTCTCTCTCTGTCACCTTGAGGGCACTGTGACTCTGTCA 2700  
 DB 2641 TGTGGCTCCAGTGTCTCTCTCTCTGTCACCTTGAGGGCACTGTGACTCTGTCA 2700  
 QY 2701 TTTTAACTCAGGTGGACCCAGGGCGAATGGGGCCAGAGCCCTTCAAGGGCAGAG 2760  
 DB 2701 TTTTAACTCAGGTGGACCCAGGGCGAATGGGGCCAGAGCCCTTCAAGGGCAGAG 2760  
 QY 2761 CCTGGCGAGAGAGAGCCCTTTGCCAGAGCAGCAGAGAGCTGCTTACTTGAACC 2820  
 DB 2761 CCTGGCGAGAGAGAGCCCTTTGCCAGAGCAGCAGAGAGCTGCTTACTTGAACC 2820  
 QY 2821 CG 2822  
 DB 2821 CG 2822  
 DB 2821 CG 2822

## RESULT 3

AB242865  
 ID AB242865 standard; DNA; 2822 BP.

XX AB242865;

XX 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor TM7XN1/GPR56 DNA SEQ ID NO:517.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KM G protein-coupled receptor modulator; antibody; immune-related disease;  
 KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KM immunological-related cell proliferative disease; autoimmune disease;  
 KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KM osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;  
 KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KM ulcer; gene; ds.

OS Homo sapiens.

XX W0200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX P-Psds; ABP82015.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

XX Disclosure: Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242865 to AB242866 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

Query Match 100.0%; Score 2822; DB 8; Length 2822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGAGAGGGTCTCGCTCTGTACACAGAGCTGAGAGTGGTGGTGGTCTGAT 60  
 DB 1 CGGCGAGAGGGTCTCGCTCTGTACACAGAGCTGAGAGTGGTGGTGGTCTGAT 60  
 QY 61 CGTAACTCCACCCCGGGGTTCAAGTATCTCATGCTCCAGCTCCCGAGTACGGG 120  
 DB 61 CGTAACTCCACCCCGGGGTTCAAGTATCTCATGCTCCAGCTCCCGAGTACGGG 120  
 QY 121 ATTACAGGTGTGACTTCCAAAGTACTCCGTGAGAGAAATGATCTCCCAAGTCGTG 180  
 DB 121 ATTACAGGTGTGACTTCCAAAGTACTCCGTGAGAGAAATGATCTCCCAAGTCGTG 180  
 QY 181 CTGCAAGACATCTCTTCCTGAGTCTCTTCTGTCAGAGTGGCCACCGAGCAGG 240  
 DB 181 CTGCAAGACATCTCTTCCTGAGTCTCTTCTGTCAGAGTGGCCACCGAGCAGG 240  
 QY 181 CTGCAAGACATCTCTTCCTGAGTCTCTTCTGTCAGAGTGGCCACCGAGCAGG 240  
 DB 181 CTGCAAGACATCTCTTCCTGAGTCTCTTCTGTCAGAGTGGCCACCGAGCAGG 240  
 QY 241 GGGCAGAGGAAGATTTCGCTTTCAGCCAGCGGAAACACACACAGAGAGCCTTC 300  
 DB 241 GGGCAGAGGAAGATTTCGCTTTCAGCCAGCGGAAACACACACAGAGAGCCTTC 300  
 QY 301 CACTACAAACCCACACAGACTGTGCAATTCAGAGAACTCCGAAGAGGCTTCACA 360  
 DB 301 CACTACAAACCCACACAGACTGTGCAATTCAGAGAACTCCGAAGAGGCTTCACA 360  
 QY 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCAAGGAC 420  
 DB 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCAAGGAC 420  
 QY 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGGAGTATCATCTTCTATGAC 480  
 DB 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGGAGTATCATCTTCTATGAC 480  
 QY 481 AAGCGTGAATTCTGCTGAGTGAACAAAGCTTTAGCTCTCTGCTTCAAGACAGAG 540  
 DB 481 AAGCGTGAATTCTGCTGAGTGAACAAAGCTTTAGCTCTCTGCTTCAAGACAGAG 540  
 QY 541 GAGAGCTGGCTCAGAGGCCCCCGCTGTTAGCACTTCTGTACCTCTGAGAGCCCT 600  
 DB 541 GAGAGCTGGCTCAGAGGCCCCCGCTGTTAGCACTTCTGTACCTCTGAGAGCCCT 600  
 QY 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCCAGAGTCTCCCCAC 660  
 DB 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCCAGAGTCTCCCCAC 660  
 QY 661 AGGCGCTCTCAATATCCCTCGGTGACAGTGGAGCTCAAAAGGAGCTCCAGTCTC 720  
 DB 661 AGGCGCTCTCAATATCCCTCGGTGACAGTGGAGCTCAAAAGGAGCTCCAGTCTC 720

QY	721	AGCCAGTTCCTGGAAGCATCCCCAGAAAGGCTTCAAGAGAGGCTTCGTGGCTGCCCCGGCAGC	780
Db	721	AGCCAGTTCCTGGAAGCATCCCCAGAAAGGCTTCAAGAGAGGCTTCGTGGCTGCCCCGGCAGC	780
QY	781	CAGCAGTTGCAAGAGCCTTGAAGTCCAAACTGACTCTGTAGATTCAATGAGGGGACATGGTG	840
Db	781	CAGCAGTTGCAAGAGCCTTGAAGTCCAAACTGACTCTGTAGATTCAATGAGGGGACATGGTG	840
QY	841	TCCTTCGAGAGAGACCGGATCAAGCCAGGTATGAAAGCTCCAGCCCAACAGCCGGCTC	900
Db	841	TCCTTCGAGAGAGACCGGATCAAGCCAGGTATGAAAGCTCCAGCCCAACAGCCGGCTC	900
QY	901	CAGGACCTGCACATCTCACTCCCGGAGGAGGAGAGCAGAGCAGATCATGAGATCTCG	960
Db	901	CAGGACCTGCACATCTCACTCCCGGAGGAGGAGAGCAGAGCAGATCATGAGATCTCG	960
QY	961	GTGCTGCTGCTCGAACACTTTCACAGAGCAGAAAGGCCGAGCCGGAGAGGCTGAGAA	1020
Db	961	GTGCTGCTGCTCGAACACTTTCACAGAGCAGAAAGGCCGAGCCGGAGAGGCTGAGAA	1020
QY	1021	AGACTCCCTCCGTGGGACTTTCAGAGCGCAAGCCCGTTCCAGGACAAAGATTCCAGGCAA	1080
Db	1021	AGACTCCCTCCGTGGGACTTTCAGAGCGCAAGCCCGTTTCAGGACAAAGATTCCAGGCAA	1080
QY	1081	GTCTCGGGTGAAGAAAGTCTTGAGGATTTGTGTTACAAACACAAAGTAGCCACCTCAGC	1140
Db	1081	GTCTCGGGTGAAGAAAGTCTTGAGGATTTGTGTTACAAACACAAAGTAGCCACCTCAGC	1140
QY	1141	GAGCCCGGTGGTCTCATCTTTCAGACCAAGCTACAGCCGGAAGATGTGACCTTGCAATGT	1200
Db	1141	GAGCCCGGTGGTCTCATCTTTCAGACCAAGCTACAGCCGGAAGATGTGACCTTGCAATGT	1200
QY	1201	GTGTTCTGGGTTGAAGACCCCAACTTGAAGACCCCGGGGCAATTGAGCAGTCTGGGGTGT	1260
Db	1201	GTGTTCTGGGTTGAAGACCCCAACTTGAAGACCCCGGGGCAATTGAGCAGTCTGGGGTGT	1260
QY	1261	GAGACCTGCAGAGAGAAACCCAAACATCTGCTTCTGCAACCACTTGACCTTCTTGCA	1320
Db	1261	GAGACCTGCAGAGAGAAACCCAAACATCTGCTTCTGCAACCACTTGACCTTCTTGCA	1320
QY	1321	GTGCTGATGAGTCTCCTCGGTGAGGTGAGACGCCGTCACAAGACACTGAGGCTCCTC	1380
Db	1321	GTGCTGATGAGTCTCCTCGGTGAGGTGAGACGCCGTCACAAGACACTGAGGCTCCTC	1380
QY	1381	TCCTACGTGGGCTGTGTGTCTCTGACCCTTGCGCTGCCTCTGTCACCAATGTCGGCTTACTCTC	1440
Db	1381	TCCTACGTGGGCTGTGTGTCTCTGACCCTTGCGCTGCCTCTGTCACCAATGTCGGCTTACTCTC	1440
QY	1441	TGCTCCAGAGGTGCCCCCTGCGGTGAGAGAGAAACCTCGGGACTACCACTAAGAGTGAC	1500
Db	1441	TGCTCCAGAGGTGCCCCCTGCGGTGAGAGAGAAACCTCGGGACTACCACTAAGAGTGAC	1500
QY	1501	ATGAACCTGCTGCTGGCGCTCTTCTGTCGTGACAGAGCTTCTGCTCAGAGCAGCCGGT	1560
Db	1501	ATGAACCTGCTGCTGGCGCTCTTCTGTCGTGACAGAGCTTCTGCTCAGAGCAGCCGGT	1560
QY	1561	GCCCTGACAGAGCTCTGAGAGCTGAGCTGCGGAGCAAGTGCACATCTTCTGCACTTCTCCTG	1620
Db	1561	GCCCTGACAGAGCTCTGAGAGCTGAGCTGCGGAGCAAGTGCACATCTTCTGCACTTCTCCTG	1620
QY	1621	CTCACCTGCTTCTCTGATGAGGCTTCAGAGGGTACAACTCTACCACTGCTGTGTGAG	1680
Db	1621	CTCACCTGCTTCTCTGATGAGGCTTCAGAGGGTACAACTCTACCACTGCTGTGTGAG	1680
QY	1681	GTCTTTGGCACTTATGTCCCTGCTACTCACTCAAGCTGAGGGCCATGGGCTGGGGCTTC	1740
Db	1681	GTCTTTGGCACTTATGTCCCTGCTACTCACTCAAGCTGAGGGCCATGGGCTGGGGCTTC	1740
QY	1741	CCCATCTTTCTGTGACGTGTGTGACCCGTGAGTGTGACAACTTATGAGCCCATATC	1800
Db	1741	CCCATCTTTCTGTGACGTGTGTGACCCGTGAGTGTGACAACTTATGAGCCCATATC	1800
QY	1801	TTGGCTGTGACATGAGCTTCAGAGGGCGTCACTCACTTCATGCTGTGATCCGGAGC	1860

Db	1801	TTGGCTGTGATAGAGACTCGAAGGGGGTCACTTACCTTCCATGTGAGTACCCGGAC	1860
QY	1861	TCCTGTGACGCTACATCAACCACTGGGGCTCTTCAAGCTGGTGTTCGTTCACATG	1920
Db	1861	TCCTGTGACGCTACATCAACCACTGGGGCTCTTCAAGCTGGTGTTCGTTCACATG	1920
QY	1921	GGCATGTGACCAACATGATGATGACAGATCTCGGCTGGCGGCCCAACCCAAAGTGG	1980
Db	1921	GGCATGTGACCAACATGATGATGACAGATCTCGGCGGTGGGCCCAACCCAAAGTGG	1980
QY	1981	TCACATGTGTGACACTGTGGGCTCAAGCTGTCTTGGCTGTGGCTGGGGCTTGATC	2040
Db	1981	TCACATGTGTGACACTGTGGGCTCAAGCTGTCTTGGCTGTGGCTGGGGCTTGATC	2040
QY	2041	TTCTTTCCTTTGGCTTGTGACACTTCCAGCTGTGTGTCTCTACCTTTTCAGCATATC	2100
Db	2041	TTCTTTCCTTTGGCTTGTGACACTTCCAGCTGTGTGTCTCTACCTTTTCAGCATATC	2100
QY	2101	ACCTCTTCCAGGGCTTCTCATCTTCACTGTGTACTGTCTCATGCGGCTGCAAGGCCG	2160
Db	2101	ACCTCTTCCAGGGCTTCTCATCTTCACTGTGTACTGTGTCTCATGCGGCTGCAAGGCCG	2160
QY	2161	GGTGGCCCCCTCCCCCTGAAAGAGCACTGACGCGGCGAAGGCTCCCACTCAGCTCGAGC	2220
Db	2161	GGTGGCCCCCTCCCCCTGAAAGAGCACTGACGCGGCTCCCACTCAGCTCGAGC	2220
QY	2221	AGCAGCTGTGTCCAGCCGCGCATCTTAGGCTCTCAGGCCCATCTGCCATGTATGAAAGCAGAA	2280
Db	2221	AGCAGCTGTGTCCAGCCGCGCATCTTAGGCTCTCAGGCCCATCTGCCATGTATGAAAGCAGAA	2280
QY	2281	TGCGGGCTCTGTGTGACACTGTGTGGGGCCCCCGAGCGAGGCCAGGCCAGGCGCAGT	2340
Db	2281	TGCGGGCTCTGTGTGACACTGTGTGGGGCCCCCGAGCGAGGCCAGGCCAGGCGCAGT	2340
QY	2341	CCGAGACTTTTGGAAAGCCCAACGACATGAGAGAGATGGGCCGTTGCAATGTGTGACGA	2400
Db	2341	CCGAGACTTTTGGAAAGCCCAACGACATGAGAGAGATGGGCCGTTGCAATGTGTGACGA	2400
QY	2401	CTCCCGGGGCTGGGGCTTTTGAATTGGCTTTGGGAACTACTCGGCTCTCATAGCTGCC	2460
Db	2401	CTCCCGGGGCTGGGGCTTTTGAATTGGCTTTGGGAACTACTCGGCTCTCATAGCTGCC	2460
QY	2461	ACGGGACTCAGAAATGCGCGGCGCATGTGCTCTAGGGTACTGTGCCCATCTGTGCCAAC	2520
Db	2461	ACGGGACTCAGAAATGCGCGGCGCATGTGCTCTAGGGTACTGTGCCCATCTGTGCCAAC	2520
QY	2521	CGAGCTGAGGCTGTGTCTCTCTTACACCCCTTGGGCCCAAGCTCTCATGTGTGGGGCCA	2580
Db	2521	CGAGCTGAGGCTGTGTCTCTCTTACACCCCTTGGGGCCAAGCTCTCATGTGTGGGGCCA	2580
QY	2581	GGCCTTGGATCTTGAAGGCTGTGGAACATCTTAACTCTGTGCCCCCTGCTGGGACAGAAA	2640
Db	2581	GGCCTTGGATCTTGAAGGCTGTGGAACATCTTAACTCTGTGCCCCCTGCTGGGACAGAAA	2640
QY	2641	TGTGGCTTCAGTGTCTGTCTCTGTGTGTCACTTGAAGGCACTTGTGATCTCTGTGCA	2700
Db	2641	TGTGGCTTCAGTGTCTGTCTCTGTGTGTCACTTGAAGGCACTTGTGATCTCTGTGCA	2700
QY	2701	TTTTTAACCTCAGGTGTGCAACCAAGGGCGAATGGGGCCAGAGCACTTCAAGGCGCAGAG	2760
Db	2701	TTTTTAACCTCAGGTGTGCAACCAAGGGCGAATGGGGCCAGAGCACTTCAAGGCGCAGAG	2760
QY	2761	CCCTGGCGAGAGAGGCGCTTGTGCAAGAGACAGCAGCAGCTTCAGCTCTGAGGC	2820
Db	2761	CCCTGGCGAGAGAGGCGCTTGTGCAAGAGACAGCAGCAGCTTCAGCTCTGAGGC	2820
QY	2821	CG 2822	
Db	2821	CG 2822	

## RESULTS

ADAI4217  
ID ADAI4217 standard; cDNA; 2822 BP.  
AC ADAI4217;  
XX  
XX  
XX 06-NOV-2003 (first entry)  
DE Human GPR56-1 encoding cDNA SEQ ID NO:1.  
XX  
XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
XX gene therapy; gene; ss.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 163..2244  
FT /tag= a  
FT /product= "GPR56-1"  
XX  
XX MO2003068965-A1.  
XX  
XX 21-AUG-2003.  
XX  
XX 12-FEB-2003; 2003MO-AUD00178.  
XX  
XX 12-FEB-2002; 2002JUS-00073054.  
XX  
XX (GTWO-) G2 THERAPIES LTD.  
XX  
XX Herzog H, Sutherland RL, Mackay CR, Henhall S;  
XX WPI, 2003-689676/65.  
XX P-PSDB; ADAI4218.  
XX  
XX New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
PT useful for preparing a composition for preventing, inhibiting or delaying  
PT tumor growth.  
XX  
XX Claim 1; Page 88-92; 129pp; English.  
XX  
XX The present invention describes a nucleic acid probe for detecting RNA  
XX encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
XX sample. Also described: (1) detecting a cancer cell in a subject; (2)  
XX detecting ovarian cancer or its metastases in a subject; (3) determining  
XX an effector memory T cell response in a subject; (4) determining whether  
XX or not a subject has been re-infected with an infectious agent; (5)  
XX determining the presence of effector memory T cells in a test sample; (6)  
XX counting effector memory T cells in a subject; (7) detecting a cancer  
XX cell in a subject; (8) reducing or preventing an inflammatory response in  
XX a subject; (9) preventing, inhibiting or delaying tumour growth in a  
XX subject; and (10) stimulating an immune response in a subject. GPR56 has  
XX cytostatic activity, and can be used in gene therapy. The nucleic acid  
XX probe is useful for preparing a composition for preventing, inhibiting or  
XX delaying tumour growth. The present sequence encodes the human GPCR,  
XX designated GPR56-1, which is used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 2822; DB 9; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGACGACAGGCTCTGCTCTGTCACACAGGCTGAGTGCAGTGGTGTATCTTGGTCAAT 60  
DB 1 CGGACGACAGGCTCTGCTCTGTCACACAGGCTGAGTGCAGTGGTGTATCTTGGTCAAT 60  
QY 61 CGTAACTTCACCTCCCGGCTTCAAGTATCTCATGCTCAGCTCCCGAGTATGCTGG 120  
DB 61 CGTAACTTCACCTCCCGGCTTCAAGTATCTCATGCTCAGCTCCCGAGTATGCTGG 120  
QY 121 ATTACAGTGTGATCTTCCAGAGTATCTCCGTGAGAGAAATGACTCCCGATGCTG 180

DB 121 ATTACAGTGTGATCTTCCAGAGTATCTCCGTGAGAGAAATGACTCCCGATGCTG 180  
QY 181 CTGACAGACGACACTGTTCTGCTGAGTCTGCTCTTCTGCTCAGGTGCCACGGCAGG 240  
DB 181 CTGACAGACGACACTGTTCTGCTGAGTCTGCTCTTCTGCTCAGGTGCCACGGCAGG 240  
QY 241 GGGCAGAGGAGAACTTTGCTTCTGACAGCCAGCGGAAACCAACACAGAGAGAGCTC 300  
DB 241 GGGCAGAGGAGAACTTTGCTTCTGACAGCCAGCGGAAACCAACACAGAGAGAGCTC 300  
QY 301 CACTAACAACCCACACACAGCCTGGCATCTTCATGAGAACTCCGAGAGAGCCCTACA 360  
DB 301 CACTAACAACCCACACACAGCCTGGCATCTTCATGAGAACTCCGAGAGAGCCCTACA 360  
QY 361 GTCCATGCCCCCTTCCCTGAGCCACCCCTGCTTCCGATCTTCCCTGACCCCAAGGGG 420  
DB 361 GTCCATGCCCCCTTCCCTGAGCCACCCCTGCTTCCGATCTTCCCTGACCCCAAGGGG 420  
QY 421 CTCTACCACTTCTGCTCTTCTGAGAAACCCGACATGCTGGAGATTAATCTTCTATG 480  
DB 421 CTCTACCACTTCTGCTCTTCTGAGAAACCCGACATGCTGGAGATTAATCTTCTATG 480  
QY 481 AAGGTGACCTTCTGCTGAGTGAACAAAGCTTACCTCTCTGCTTCCAGACAGAG 540  
DB 481 AAGGTGACCTTCTGCTGAGTGAACAAAGCTTACCTCTCTGCTTCCAGACAGAG 540  
QY 541 GAGAGCTGCTCAGAGCCGCCCTGTTAGCCACTTCTGCTCAGCTCTGCTGAGAGCC 600  
DB 541 GAGAGCTGCTCAGAGCCGCCCTGTTAGCCACTTCTGCTCAGCTCTGCTGAGAGCC 600  
QY 541 GAGAGCTGCTCAGAGCCGCCCTGTTAGCCACTTCTGCTCAGCTCTGCTGAGAGCC 600  
DB 541 GAGAGCTGCTCAGAGCCGCCCTGTTAGCCACTTCTGCTCAGCTCTGCTGAGAGCC 600  
QY 601 CAGAAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 601 CAGAAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
QY 661 ACGGCGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
DB 661 ACGGCGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
QY 721 AGCGATTCCTGAGACATCCCGAGAGGCTTCAAGAGAGGCTTCCGCTGCTGCTGCTG 780  
DB 721 AGCGATTCCTGAGACATCCCGAGAGGCTTCAAGAGAGGCTTCCGCTGCTGCTGCTG 780  
QY 781 CAGCAGTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 CAGCAGTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 841 TCCCTGAGAGAGAGCCGATCAACGCTGATGAAAGCTTCCAGCCACAGCCGCTC 900  
DB 841 TCCCTGAGAGAGAGCCGATCAACGCTGATGAAAGCTTCCAGCCACAGCCGCTC 900  
QY 901 CAGGACCTGACATTCATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
DB 901 CAGGACCTGACATTCATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 961 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
DB 961 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
QY 1021 AGACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
DB 1021 AGACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
QY 1081 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
DB 1081 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
QY 1141 GAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
DB 1141 GAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
QY 1201 GTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260



Db 1201 GTGTTCTGAGTTGAGAGACCCCAATTGAGCAGCCCGGAGCATTTGAGCAGTGTGAGTGT 1260  
 QY 1261 GAGACCGGTGAGAGAGAGAAACCAACATCTGCTTGTGAAACCACTTGAACCTTATGCA 1320  
 Db 1261 GAGACCGGTGAGAGAGAGAAACCAACATCTGCTTGTGAAACCACTTGAACCTTATGCA 1320  
 QY 1321 GTGCTGATGATCTCTCGGTGAGGTGAGACCGGTGCAACAGCACTTGAACCTTCTC 1380  
 Db 1321 GTGCTGATGATCTCTCGGTGAGGTGAGACCGGTGCAACAGCACTTGAACCTTCTC 1380  
 QY 1381 TCTCTAGTGGGCTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 Db 1381 TCTCTAGTGGGCTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 QY 1441 TCTCTAGTGGGCTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 Db 1441 TCTCTAGTGGGCTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 QY 1501 ATGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 Db 1501 ATGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 QY 1561 GGCCTGACAGGCTCTGAGGCTGAGCTGAGCCAGAGTGCATCTTCTGCTGCTGCTGCTGCTGCT 1620  
 Db 1561 GGCCTGACAGGCTCTGAGGCTGAGCTGAGCCAGAGTGCATCTTCTGCTGCTGCTGCTGCTGCT 1620  
 QY 1621 CTCACCTGCTCTTCTGATGAGGCTCTGAGGAGTACAACTCTTACCGACTGCTGCTGCTGCTGCT 1680  
 Db 1621 CTCACCTGCTCTTCTGATGAGGCTCTGAGGAGTACAACTCTTACCGACTGCTGCTGCTGCTGCT 1680  
 QY 1681 GTCTTTGGGACCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 Db 1681 GTCTTTGGGACCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 QY 1741 CCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
 Db 1741 CCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
 QY 1801 TTGGCTGTGATGAGTACCTCAAGAGGCTGATCTTACCTTTCATGCTGCTGCTGCTGCTGCTGCT 1860  
 Db 1801 TTGGCTGTGATGAGTACCTCAAGAGGCTGATCTTACCTTTCATGCTGCTGCTGCTGCTGCTGCT 1860  
 QY 1861 TCCCTGTGAGCTACATCAACCACTGAGGCTCTTCAAGCTGAGTGTCTGCTGCTGCTGCTGCTGCT 1920  
 Db 1861 TCCCTGTGAGCTACATCAACCACTGAGGCTCTTCAAGCTGAGTGTCTGCTGCTGCTGCTGCTGCT 1920  
 QY 1921 GCCATGTAGCAACCATGTGTGAGATCTGCGGCTGCGCCCAACCCCAAGAGTGG 1980  
 Db 1921 GCCATGTAGCAACCATGTGTGAGATCTGCGGCTGCGCCCAACCCCAAGAGTGG 1980  
 QY 1981 TCAATGTGTGACATGCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
 Db 1981 TCAATGTGTGACATGCTGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
 QY 2041 TTCTTCTCTTGTGCTTGTGCACTTCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
 Db 2041 TTCTTCTCTTGTGCTTGTGCACTTCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
 QY 2101 ACCCTCTTCAAGGCTTCTCATCTTCACTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
 Db 2101 ACCCTCTTCAAGGCTTCTCATCTTCACTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
 QY 2161 GGTGGGCTCTCTCTGAGAGAGCACTGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2220  
 Db 2161 GGTGGGCTCTCTCTGAGAGAGCACTGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2220  
 QY 2221 AGCACTGTCTCAAGCTGATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 2280  
 Db 2221 AGCACTGTCTCAAGCTGATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 2280  
 QY 2281 TGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
 Db 2281 TGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340

QY 2341 CCGCAGACTTTGAGAAACCCCAACGACCATGAGAGATGGGCGCTTGCATGCTGAGCAGA 2400  
 Db 2341 CCGCAGACTTTGAGAAACCCCAACGACCATGAGAGATGGGCGCTTGCATGCTGAGCAGA 2400  
 QY 2401 CTCCTGGGCTGAGGCTTTTGAATTGGCTTGGAGGACTACTGAGCTCTGCTGAGCTGCC 2460  
 Db 2401 CTCCTGGGCTGAGGCTTTTGAATTGGCTTGGAGGACTACTGAGCTCTGCTGAGCTGCC 2460  
 QY 2461 ACAGGACTGAGAGTGCAGGCTGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 2520  
 Db 2461 ACAGGACTGAGAGTGCAGGCTGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 2520  
 QY 2521 CCAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
 Db 2521 CCAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
 QY 2581 GGCCTGAGATCTTGAAGGCTGAGCACTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 Db 2581 GGCCTGAGATCTTGAAGGCTGAGCACTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 QY 2641 TGTGCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 Db 2641 TGTGCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 QY 2701 TTTTAACTTCAAGTGTGCAACCAAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2760  
 Db 2701 TTTTAACTTCAAGTGTGCAACCAAGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2760  
 QY 2761 CCCTGGCGAGAGAGAGGCTTTTGCAGAGAGCAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 Db 2761 CCCTGGCGAGAGAGGCTTTTGCAGAGAGCAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 QY 2821 CG 2822  
 Db 2821 CG 2822

RESULT 5  
 AAX25359  
 ID AAX25359 standard, cDNA; 2834 BP.  
 XX AAX25359;  
 XX  
 AC  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Human G protein coupled receptor TSR32 cDNA.  
 XX  
 KW TSR32; G protein coupled receptor; thyroid; human; Bardet Biedl syndrome;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS  
 FT /\*tag= a  
 FT  
 XX  
 PN W09915551-A1.  
 XX  
 PD 01-APR-1999.  
 XX  
 PF 24-SEP-1998; 98W0-AU000805.  
 PR 24-SEP-1997; 97AU-00009386.  
 XX  
 PA (GARV-) GARVAN INST MEDICAL RES.  
 XX  
 PI Herzog H;  
 XX  
 DR WPI; 1999-244386/20.  
 DR P-PSDB; AAY05730.  
 XX  
 FT New G-protein-coupled receptor designated TSR32.

XX Claim 5; 10-11; 23bp; English.

XX This is the nucleotide sequence of an isolated polynucleotide, the coding  
XX region of which is also claimed, encoding a new human G protein coupled  
CC receptor, termed TSR32 (see AAY05730), which is a member of the secretin  
CC receptor family. TSR32 is expressed in many tissue types, with highest  
CC expression in the thyroid gland, suggesting that TSR32 has important  
CC functions in metabolic regulation throughout the body via the thyroid  
CC gland. TSR32 cDNA was isolated from a human heart cDNA library using a  
CC 456 bp fragment that had itself identified using degenerate  
CC oligonucleotides based on conserved regions of the human glucagon-like  
CC peptide receptor family. The invention provides TSR32 polypeptides,  
CC polynucleotides, a vector, host cells, an antibody and a non-human  
CC transgenic animal, as well as a method for detecting agonists or  
CC antagonists of TSR32, oligonucleotide or polynucleotide probes, an  
CC antisense polynucleotide, and a method of producing TSR32 or its agonists  
CC and antagonists by culturing the host cells. The TSR32 protein, its agonists  
CC and antagonists can be used to regulate thyroid functions in growth,  
CC development and metabolic activity. The gene for TSR32 has been mapped to  
CC chromosome 16q31, where Bardet Biedl syndrome, an autosomal recessive  
CC disorder, has been linked

SQ Sequence 2834 BP; 520 A; 951 C; 767 G; 596 T; 0 U; 0 Other;

Query Match 100.0%; Score 2822; DB 2; Length 2834;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACAGAGGTCCTGCTGTCACACAGGCTGAGTGCAGTGTGATTTGGCTCAT 60  
DB 7 CGGACAGAGGTCCTGCTGTCACACAGGCTGAGTGCAGTGTGATTTGGCTCAT 66  
QY 61 CGTAACTTCAACCTCCGGGTTCAAGTATTCATGCTCAGGCTCCGAGTACGCTG 120  
DB 67 CGTAACTTCAACCTCCGGGTTCAAGTATTCATGCTCAGGCTCCGAGTACGCTG 126  
QY 121 ATTACAGGTGATGATTCAGAGTGAATCCGTCGAGGAAATGACTCCCACTGCTG 180  
DB 127 ATTACAGGTGATGATTCAGAGTGAATCCGTCGAGGAAATGACTCCCACTGCTG 186  
QY 181 CTGACAGACGACCTGCTGCTGATGATGCTCTTCTGCTGTCAGAGTGCCTCAGG 240  
DB 187 CTGACAGACGACCTGCTGCTGATGATGCTCTTCTGCTGTCAGAGTGCCTCAGG 246  
QY 241 GGCCACAGGGAAGCTTGGCTGTCGACGAGCGGAAACAGACACAGAGAGGCTC 300  
DB 247 GGCCACAGGGAAGCTTGGCTGTCGACGAGCGGAAACAGACACAGAGAGGCTC 306  
QY 301 CACTACAAACCCACACAGACCTGCGATCTTCATGAGAACTCCGAAAGGCTTCA 360  
DB 307 CACTACAAACCCACACAGACCTGCGATCTTCATGAGAACTCCGAAAGGCTTCA 366  
QY 361 GTCCATGCCCCCTTCCCTGACGCCACCTGCTTCCGATCCCTGACCCGAGG 420  
DB 367 GTCCATGCCCCCTTCCCTGACGCCACCTGCTTCCGATCCCTGACCCGAGG 426  
QY 421 CTACACACTTCTGCTCTACTGAAACCAAGCATGCTGGAGATTACATCTTCTATG 480  
DB 427 CTACACACTTCTGCTCTACTGAAACCAAGCATGCTGGAGATTACATCTTCTATG 486  
QY 481 AAGCGTGACTTCTGCTGATGAGCAAAAGCTTACGCTCTGCTTCAAGACCAAG 540  
DB 487 AAGCGTGACTTCTGCTGATGAGCAAAAGCTTACGCTCTGCTTCAAGACCAAG 546  
QY 541 GAGAGCTGGCTCAGAGGCCCCCGCTGTAGCACTTGTACCTCTGAGTGAAGCT 600  
DB 547 GAGAGCTGGCTCAGAGGCCCCCGCTGTAGCACTTGTGTACCTCTGAGTGAAGCT 606  
QY 601 CAGAACATCAGCTGCCAGTGCAGCAGAGCTTCACTTCTCTTCCACAGTCTCCCA 660  
DB 607 CAGAACATCAGCTGCCAGTGCAGCAGAGCTTCACTTCTCTTCCACAGTCTCCCA 666

QY 661 ACGGCGCTCAACATGCTGCTGAGCATGTGAGACTCAAAAGGAGCTCAGCTGCTC 720  
DB 667 ACGGCGCTCAACATGCTGCTGAGCATGTGAGACTCAAAAGGAGCTCAGCTGCTC 726  
QY 721 AGCCAGTTCCTGAAGCATCCCGAAGAGGCTTCAAGAGGCTCAGCTGCTCCCGCAGC 780  
DB 727 AGCCAGTTCCTGAAGCATCCCGAAGAGGCTTCAAGAGGCTCAGCTGCTCCCGCAGC 786  
QY 781 CAGCAGTTCGAGAGCTGAGTGAATCTGACCTCTGTGATTCATGTGGGACATGAGT 840  
DB 787 CAGCAGTTCGAGAGCTGAGTGAATCTGACCTCTGTGATTCATGTGGGACATGAGT 846  
QY 841 TCCCTGAGAGAGACCGGATCAACGCGAGGTATGAAAGCTCCAGCCACAGCGGCTC 900  
DB 847 TCCCTGAGAGAGACCGGATCAACGCGAGGTATGAAAGCTCCAGCCACAGCGGCTC 906  
QY 901 CAGAGCTTCGACATCCATCCCGCAGAGAGAGAGAGAGAGATCATGAGTACTCG 960  
DB 907 CAGAGCTTCGACATCCATCCCGCAGAGAGAGAGAGAGAGATCATGAGTACTCG 966  
QY 961 GTGCTGCTGCTGAGACATCTTTCAGAGAGCCAAAGCCGAGGCGGAGGCTGAGAG 1020  
DB 967 GTGCTGCTGCTGAGACATCTTTCAGAGAGCCAAAGCCGAGGCGGAGGCTGAGAG 1026  
QY 1021 AGACTCCTCCGTTGAGACTTCAGAGCCAAAGCCCTGTTCCAGACCAAGATTCCAGCAA 1080  
DB 1027 AGACTCCTCCGTTGAGACTTCAGAGCCAAAGCCCTGTTCCAGACCAAGATTCCAGCAA 1086  
QY 1081 GTCTGAGTGAAGAGTCTTGGAGATTGTGTACAGAACACCAAGTACCACTTCA 1140  
DB 1087 GTCTGAGTGAAGAGTCTTGGAGATTGTGTACAGAACACCAAGTACCACTTCA 1146  
QY 1141 GAGCCCTGCTGCTCACTTTCACACACAGTACAGCCGAGAAATGATCTGCAATGT 1200  
DB 1147 GAGCCCTGCTGCTCACTTTCACACACAGTACAGCCGAGAAATGATCTGCAATGT 1206  
QY 1201 GTGTTGAGGTTGAAGACCCCAATGAGACGCCGAGGCAATGAGAGTGTGAGT 1260  
DB 1207 GTGTTGAGGTTGAAGACCCCAATGAGACGCCGAGGCAATGAGAGTGTGAGT 1266  
QY 1261 GAGACCGTCAGAGAGAAACCCAAACATCTGCTTCTGCAACCACTTGAACCTTTCGA 1320  
DB 1267 GAGACCGTCAGAGAGAAACCCAAACATCTGCTTCTGCAACCACTTGAACCTTTCGA 1326  
QY 1321 GTGCTGATGCTCTCGGTGAGAGTGAAGCCGTCGACCAAGACTACCTGAGCTCCTC 1380  
DB 1327 GTGCTGATGCTCTCGGTGAGAGTGAAGCCGTCGACCAAGACTACCTGAGCTCCTC 1386  
QY 1381 TCTTACGTGGCTGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440  
DB 1387 TCTTACGTGGCTGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446  
QY 1441 TGTCTCAGAGTGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
DB 1447 TGTCTCAGAGTGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506  
QY 1501 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
DB 1507 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1566  
QY 1561 GGCCTGACAGGCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
DB 1567 GGCCTGACAGGCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1626  
QY 1621 CTACCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
DB 1627 CTACCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686  
QY 1681 GTCTTGGACCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
DB 1687 GTCTTGGACCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746  
QY 1741 CCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800

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Db      1747  CCCATCTTCTGCTGAGCGCTGTGGCCCTGTGGATGTGACCACTATGAGCCCATCATC
Qy      1801  TTGGCTGTGATGAGACTCCAGAGGGGCTCATCTACACCTTCCAAATGTGGATCCGGAG
Db      1807  TTGGCTGTGATGAGACTCCAGAGGGGCTCATCTACACCTTCCAAATGTGGATCCGGAG
Qy      1861  TCCCTGTGAGTACATCACTACCAACCTGGGCTCTTCCAGCTGTGTCTGTTCACATG
Db      1867  TCCCTGTGAGTACATCACTACCAACCTGGGCTCTTCCAGCTGTGTCTGTTCACATG
Qy      1921  GGCATGTAGCCACCACTGTGTGTGACATCTGTGGGCTGGGCCCCCAACCAAAATGG
Db      1927  GGCATGTAGCCACCACTGTGTGTGACATCTGTGGGCTGGGCCCCCAACCAAAATGG
Qy      1981  TCACATGTGTGACACTGTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      1987  TCACATGTGTGACACTGTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2041  TTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2047  TTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2101  ACCTCTTCCAAAGGCTTCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2107  ACCTCTTCCAAAGGCTTCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2161  GGTGGCCCTTCCCTCTGAGAGCACTGACCTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2167  GGTGGCCCTTCCCTCTGAGAGCACTGACCTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2221  AGCACTGTGTGACGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2227  AGCACTGTGTGACGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2281  TGGGCTGTGTGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2287  TGGGCTGTGTGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2341  CCGCAGACTTGTGAGAGCCCAACGACATGAGAGATGTGTGTGTGTGTGTGTGT
Db      2347  CCGCAGACTTGTGAGAGCCCAACGACATGAGAGATGTGTGTGTGTGTGTGTGT
Qy      2401  CTCCCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2407  CTCCCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2461  ACCGGACTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2467  ACCGGACTCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2521  CCACTGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2527  CCACTGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2581  GGCCTTGTGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2587  GGCCTTGTGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2641  TGTGCTCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2647  TGTGCTCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2701  TTTTAACTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2707  TTTTAACTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2761  CCGTGTGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      2767  CCGTGTGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      2821  CG 2822

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Db      2827  CG 2828
Qy      2827  CG 2828

RESULT 6
ADN39449
ID      ADN39449 standard; cDNA; 2821 BP.
XX      AC      ADN39449;
XX      DT      17-JUN-2004 (first entry)
XX      DE      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:449.
XX      KW      Human; differential expression; cancer; angiogenic disorder;
KW      fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
KW      inflammatory disease; autoimmune disease;
KW      retinal neovascularization syndrome; scarring; uterine fibroid;
KW      detection; diagnosis; prognosis; drug screening; drug targeting;
KW      wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KW      vulnery; gene therapy; vaccine; gene; ss.
XX      OS      Homo sapiens.
XX      PN      WO2003042661-A2.
XX      PD      22-MAY-2003.
XX      PP      13-NOV-2002; 2002WO-US036810.
XX      PR      13-NOV-2001; 2001US-0350666P.
XX      PR      21-NOV-2001; 2001US-0332464P.
XX      PR      29-NOV-2001; 2001US-0343933P.
XX      PR      03-DEC-2001; 2001US-0353949P.
XX      PR      14-DEC-2001; 2001US-0340376P.
XX      PR      08-JAN-2002; 2002US-0347211P.
XX      PR      10-JAN-2002; 2002US-0347349P.
XX      PR      08-FEB-2002; 2002US-0355250P.
XX      PR      13-FEB-2002; 2002US-0356714P.
XX      PR      20-FEB-2002; 2002US-0359077P.
XX      PR      29-MAR-2002; 2002US-0368809P.
XX      PR      04-APR-2002; 2002US-0370110P.
XX      PR      12-APR-2002; 2002US-0372246P.
XX      PR      05-JUN-2002; 2002US-0386614P.
XX      PR      16-JUL-2002; 2002US-0396839P.
XX      PR      22-JUL-2002; 2002US-0397755P.
XX      PR      22-JUL-2002; 2002US-0397845P.
XX      PR      09-SEP-2002; 2002US-0409450P.
XX      PA      (EOMB-) BOS BIOTECHNOLOGY INC.
XX      PI      Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezl PA;
PI      Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX      DR      WPI; 2003-468649/44.
XX      DR      P-PSDB; ADN39450.
XX      PT      Determining the presence or absence of a pathological cell in a patient,
PT      useful for diagnosing, prognosing or treating cancer, comprises detecting
PT      a nucleic acid in a biological sample.
XX      PS      Claim 8; SEQ ID NO 449; 1385bp; English.
XX      CC      The invention relates to nucleic acids and proteins (ADN38663-ADN40064)
CC      whose expression is upregulated or downregulated in specific cancers or
CC      other diseases such as angiogenic or fibrotic disorders, and to methods
CC      of determining the presence or absence of a pathological cell in a
CC      patient by detecting a nucleic acid at least 80% identical to those of
CC      the invention or by detecting a polypeptide of the invention. The
CC      invention also relates to expression vectors and host cells comprising a
CC      nucleic acid of the invention; antibodies which specifically bind a
CC      polypeptide of the invention; use of such antibodies for drug targeting;
CC      and methods of screening for modulators of activity or expression of the
CC      polypeptides and nucleic acids. The nucleic acids, polypeptides,

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CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring, and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.

XX Sequence 2821 BP, 516 A; 948 C; 765 G; 592 T; 0 U; 0 Other;

Query Match 99.9%; Score 2820; DB 11; Length 2821;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGAGGAGGGGCTGCTCTGTCACACAGGCTGAGTGCATGCTGATCTTGGCTCAT 60  
 DB 1 CGGAGGAGGGGCTGCTCTGTCACACAGGCTGAGTGCATGCTGATCTTGGCTCAT 60  
 QY 61 CGTAACTTCACTCCCGGGTTCAAGTATTTCTCATGCTCAGCCTCCGAGTACTGGG 120  
 DB 61 CGTAACTTCACTCCCGGGTTCAAGTATTTCTCATGCTCAGCCTCCGAGTACTGGG 120  
 QY 121 ATTACAGGTGTGATCTTCCAGAGTGAATCCGTCGGAAGAAATGATCCCAAGTGGCTG 180  
 DB 121 ATTACAGGTGTGATCTTCCAGAGTGAATCCGTCGGAAGAAATGATCCCAAGTGGCTG 180  
 QY 181 CTGAGAGGACACTGTTCCCTGCTGAGTGTCTCTTCTGCTGCTCAAGGTGCCACGACAG 240  
 DB 181 CTGAGAGGACACTGTTCCCTGCTGAGTGTCTCTTCTGCTGCTCAAGGTGCCACGACAG 240  
 QY 241 GGGCAAGGGAAGACTTGGCTTCTGAGCCAGCCAGCCAGACACACACACAGAGAGCTTC 300  
 DB 241 GGGCAAGGGAAGACTTGGCTTCTGAGCCAGCCAGCCAGACACACACAGAGAGCTTC 300  
 QY 301 CACTCAAAACCAACCAACCAACCTGCGCATCTCCATGAGAGAACTCCGAGAGGCTTCACA 360  
 DB 301 CACTCAAAACCAACCAACCAACCTGCGCATCTCCATGAGAGAACTCCGAGAGGCTTCACA 360  
 QY 361 GTCCATGCCCCCTTCCCTGAGCCACCTGCTTCCGATCTTCCCTGACCCACAGGGGCT 420  
 DB 361 GTCCATGCCCCCTTCCCTGAGCCACCTGCTTCCGATCTTCCCTGACCCACAGGGGCT 420  
 QY 421 CTCTACCACTTCTGCTCTTCTGAGAACCGACATGCTGGAGATTAATCTTCTCTATGGC 480  
 DB 421 CTCTACCACTTCTGCTCTTCTGAGAACCGACATGCTGGAGATTAATCTTCTCTATGGC 480  
 QY 481 AAGCGGACCTTCTGCTGAGTGAACAAAGCTCTAGCCTCTGCTGCTCCAGACACAGAG 540  
 DB 481 AAGCGGACCTTCTGCTGAGTGAACAAAGCTCTAGCCTCTGCTGCTCCAGACACAGAG 540  
 QY 541 GAGAGCTGGCTCAGGGGCCCCCGCTGTTAGCCACTTCTGTCACTCTGCTGGAGGCTCT 600  
 DB 541 GAGAGCTGGCTCAGGGGCCCCCGCTGTTAGCCACTTCTGTCACTCTGCTGGAGGCTCT 600  
 QY 601 CAGAACATCAGCTGCCCCAGTGGCCGACGCTTCACTTCTCTTCCACAGCTCTCCAC 660  
 DB 601 CAGAACATCAGCTGCCCCAGTGGCCGACGCTTCACTTCTCTTCCACAGCTCTCCAC 660  
 QY 661 AAGGCGGCTCAAGATGCTGAGTGAACATGTCGAGTCAAAAGGAGCTTCAAGTCTCTC 720  
 DB 661 AAGGCGGCTCAAGATGCTGAGTGAACATGTCGAGTCAAAAGGAGCTTCAAGTCTCTC 720  
 QY 721 AGGCAATTCCTGAAGATCCCAAGAGGCTTCAAGAGGCTCTGCTGGCTGCCGACAGC 780  
 DB 721 AGGCAATTCCTGAAGATCCCAAGAGGCTTCAAGAGGCTCTGCTGGCTGCCGACAGC 780  
 QY 781 CAGCAGTTGAGAGCTGAGTGAACATGATCTCTGAGATTCATGAGGAGGAGCATGCTG 840  
 DB 781 CAGCAGTTGAGAGCTGAGTGAACATGATCTCTGAGATTCATGAGGAGGAGCATGCTG 840  
 QY 841 TCTCTGAGAGAGCCGATCAACGACGCTATGAGAGCTTCAAGCCACAGCCGAGCTTC 900  
 DB 841 TCTCTGAGAGAGCCGATCAACGACGCTATGAGAGCTTCAAGCCACAGCCGAGCTTC 900

QY 901 CAGACCTTGCACTTCCATCCCGGAGAGAGAGAGAGAGAGATGATGAGATCTG 960  
 DB 901 CAGACCTTGCACTTCCATCCCGGAGAGAGAGAGAGAGAGATGATGAGATCTG 960  
 QY 961 GTGCTGCTGCTCCGAACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
 DB 961 GTGCTGCTGCTCCGAACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
 QY 1021 AGACTCTCTGCTGAGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 DB 1021 AGACTCTCTGCTGAGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 QY 1081 GTCTGCTGAG 1140  
 DB 1081 GTCTGCTGAG 1140  
 QY 1141 GAGCCGAG 1200  
 DB 1141 GAGCCGAG 1200  
 QY 1201 GTGCTGCTGAG 1260  
 DB 1201 GTGCTGCTGAG 1260  
 QY 1261 GAGACCTGAG 1320  
 DB 1261 GAGACCTGAG 1320  
 QY 1321 GTGCTGATGATCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
 DB 1321 GTGCTGATGATCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
 QY 1381 TCTCTAGTGGTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 DB 1381 TCTCTAGTGGTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 QY 1441 TCTCTAGTGGTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 DB 1441 TCTCTAGTGGTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 QY 1501 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 DB 1501 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 QY 1561 GCTCTGAG 1620  
 DB 1561 GCTCTGAG 1620  
 QY 1621 CTGACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 DB 1621 CTGACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 1681 GTCTTGGAG 1740  
 DB 1681 GTCTTGGAG 1740  
 QY 1741 CCAATCTTCTGAG 1800  
 DB 1741 CCAATCTTCTGAG 1800  
 QY 1801 TTGCTGCTGAG 1860  
 DB 1801 TTGCTGCTGAG 1860  
 QY 1861 TCCCTGCTGAG 1920  
 DB 1861 TCCCTGCTGAG 1920  
 QY 1921 GCTATGCTGAG 1980  
 DB 1921 GCTATGCTGAG 1980  
 QY 1981 TCACATGCTGAG 2040  
 DB 1981 TCACATGCTGAG 2040



QY 182 TCGAGAGACACTGTTCTGTGTGAGTGTGCTCTTCTGTGTCAAGTGTCCCAAGGCGAGAGG 241  
Db 484 TCGAGAGACACTGTTCTGTGTGAGTGTGCTCTTCTGTGTCAAGTGTCCCAAGGCGAGAGG 543  
QY 242 GCCACAGGAGAGACTTTCGTCTGTGACGAGCGAGAACAGACACAGAGAGAGCTCTCC 301  
Db 544 GCCACAGGAGAGACTTTCGTCTGTGACGAGCGAGAACAGACACAGAGAGAGCTCTCC 603  
QY 302 ACTACAAACCACACACAGACCTGTGCAATCTTCATCGAAGACTCCGAAGAGGCTCTCAG 361  
Db 604 ACTACAAACCACACACAGACCTGTGCAATCTTCATCGAAGACTCCGAAGAGGCTCTCAG 663  
QY 362 TCGATGCCCCCTTCCCTGAGGCCCCAGCTGTCCGATCCGATCCCTGAGCCCCAGGGGCC 421  
Db 664 TCGATGCCCCCTTCCCTGAGGCCCCAGCTGTCCGATCCGATCCCTGAGCCCCAGGGGCC 723  
QY 422 TCTACCACTTCTGTCTGTATCGAACCAGCAATGTGGAGATTACATCTTCTGTATGCA 481  
Db 724 TCTACCACTTCTGTCTGTATCGAACCAGCAATGTGGAGATTACATCTTCTGTATGCA 783  
QY 482 AGCGTGAATTTTGTGTGATGACAAAGCTCTAGCTCTGTGTGTGCAAGAGAG 541  
Db 784 AGCGTGAATTTTGTGTGATGACAAAGCTCTAGCTCTGTGTGTGCAAGAGAG 843  
QY 542 AGAGCTGGGCTCAGGGCCCCCGCTGTAGCACTTCTGTGACCTCTGTGTGAGGCTTC 601  
Db 844 AGAGCTGGGCTCAGGGCCCCCGCTGTAGCACTTCTGTGACCTCTGTGTGAGGCTTC 903  
QY 602 AGACATCAGCTGCTCCAGTGTGCGCAGCTTCACTCTTCTTCCACAGTCTCTCCACA 661  
Db 904 AGACATCAGCTGCTCCAGTGTGCGCAGCTTCACTCTTCTTCCACAGTCTCTCCACA 963  
QY 662 CGGCGGCTCACAATGCTCTGTGTGACATGTGCGAGCTCAAAAGGAGCTTCCAGGCTCA 721  
Db 964 CGGCGGCTCACAATGCTCTGTGTGACATGTGCGAGCTCAAAAGGAGCTTCCAGGCTCA 1023  
QY 722 GCGAGTTCTGTAGAGATCCCGAGAGGCTCTCAGAGGCTCTCGGCTGCTCCCGGCGAGCC 781  
Db 1024 GCGAGTTCTGTAGAGATCCCGAGAGGCTCTCAGAGGCTCTCGGCTGCTCCCGGCGAGCC 1083  
QY 782 AGCAGTTGACAGGCTGTGAGTGTGAACTGACTCTGTGTGATTCATGTGGGGACATGTGT 841  
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KW secreted protein; transmembrane protein; ss.  
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XX  
PN WO946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-US005028.  
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RESULT 9
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OS Homo sapiens;
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PD 14-SEP-2000.
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PF 18-FEB-2000; 2000WO-US004341.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
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PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IU, Kuo SS, Napier MA, Pan J, Piont NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
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DR WPI; 2000-61443/58.
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PT F-PDB; AAB44321.
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PT Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX
PS Claim 2; Fig 203; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and BSR (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytosolic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence
XX of PRO polypeptides in samples, for linking bioactive molecules to cells
XX and for modulating biological activities of cells, using the polypeptides
XX for specific targeting. The polypeptide targeting can be used to kill the
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX provide specific targeting of bioactive molecules to cells. AAC78600 to
XX AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
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SQ Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;
Query Match 98.6%; Score 2783.4; DB 3; Length 3819;

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Best Local Similarity 99.7%; Pred. No. 0;  
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QY 1495 TCCAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1554  
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QY 1504 AACCTGTGCTGAGGCGGTCTTCTGCTGGA CAGAGCTTCTGCTGAGCAGCGGTGCTC 1563  
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QY 1555 AACCTGTGCTGAGGCGGTCTTCTGCTGGA CAGAGCTTCTGCTGAGCAGCGGTGCTC 1614  
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QY 1564 CTGAGAGCTGTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1623  
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QY 1615 CTGAGAGCTGTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1674  
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QY 1624 ACCCTCTTCTTCTGAGTGGGCTTCAGAGGGATCAACCTCTTACCGATCGTGGTGAAGT 1683  
Db |  
QY 1675 ACCCTCTTCTTCTGAGTGGGCTTCAGAGGGATCAACCTCTTACCGATCGTGGTGAAGT 1734  
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QY 1684 TTTGGACCTATGTCCCTGCTGCTACCTTCAAGCTGAGGCGCATGAGGCTTGGGCTTCC 1743  
Db |  
QY 1735 TTTGGACCTATGTCCCTGCTGCTACCTTCAAGCTGAGGCGCATGAGGCTTGGGCTTCC 1794  
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QY 1744 ATCTTCTGTGAGCGTGTGAGCCCTGTGTGAGTGTGAGCACTATATGCCCCATCATCTTG 1803  
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QY 1795 ATCTTCTGTGAGCGTGTGAGCCCTGTGTGAGTGTGAGCACTATATGCCCCATCATCTTG 1854  
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QY 1804 GCTGTGATAGAGCTTCCAGAGGCGGTCACTACCTTCCATGCTGAGATCCGAGCTCC 1863  
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QY 1855 GCTGTGATAGAGCTTCCAGAGGCGGTCACTACCTTCCATGCTGAGATCCGAGCTCC 1914  
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QY 1864 CTGAGTCAATCACTCAACCTGAGCTTTCAGGCTGTGTGTTCTGTTCACATGAGCC 1923  
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QY 1915 CTGAGTCAATCACTCAACCTGAGCTTTCAGGCTGTGTGTTCTGTTCACATGAGCC 1974  
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QY 1924 ATGCTAGCCACATGAGTGTGAGATCTGCGGCTGCGGCCCAACCCAAAGTGTGCA 1983  
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QY 1975 ATGCTAGCCACATGAGTGTGAGATCTGCGGCTGCGGCCCAACCCAAAGTGTGCA 2034  
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QY 2095 TTTCTCTTGTGCTTGTGACCTTTCAGCTTGTGTCTTCACTTTCACATGATACCC 2154  
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QY 2104 TCTTCTCAAGCTTCTCATCTGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 2163  
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Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
Query Match 98.6%; Score 2783.4; DB 4; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
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Db CTGAGGGGTCTCGCTCTGTCAACAGGCTGAGTCAAGTGTGTATCTTGGCTCATGCT 114  
64 AACCTCACTCCCGGGTTCAAGTATCTCATGCTCTAGCTCCCGATGAGTGGATT 123  
Db AACCTCACTCCCGGGTTCAAGTATCTCATGCTCTAGCTCCCGATGAGTGGATT 174  
115 AACCTCACTCCCGGGTTCAAGTATCTCATGCTCTAGCTCCCGATGAGTGGATT 174  
124 ACAGTGTGTATCTTCAAGATGACTCCGTGGAGGAAATGATCTCCCAAGTGGTGTG 183  
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175 ACAGTGTGTATCTTCAAGATGACTCCGTGGAGGAAATGATCTCCCAAGTGGTGTG 234  
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235 CAGAGACACTGTTCTGTGATGCTGCTCTTCTGTCAAGGTGCCACGGCAGGGGC 294  
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Db CACAGGGAAGATTCTGCTTGTGACGACGCGAAACAGACACACAGAGACGCTCCAC 354  
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364 CATGCCCCCTTCCCTGACAGCCCACTGCTTCCGATCTTCCCTGACCCCAAGGGGCTTC 423  
Db CATGCCCCCTTCCCTGACAGCCCACTGCTTCCGATCTTCCCTGACCCCAAGGGGCTTC 474  
415 CATGCCCCCTTCCCTGACAGCCCACTGCTTCCGATCTTCCCTGACCCCAAGGGGCTTC 474  
424 TACCACTTCTGCTCTACTGAAACGACATGCTGGAGATTAATTTCTTATGGCAAG 483  
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Db CATGTGTGACACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2094  
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QY 2104 TCCTCCAGAGGCTTCTCATCTTCACTGTGTACTGTGCATATGCGGCTGCAGGCCCCGGGT 2163  
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 ABK3602  
 ID ABK3602 standard; cDNA; 3819 BP.  
 AC ABK3602;  
 XX  
 DT 08-MAY-2002 (first entry)  
 DE cDNA encoding human PRO protein, Seq ID No 133.  
 XX  
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KM pericyte cell proliferation; chondrocyte cell proliferation;  
 KM tumour necrosis factor-alpha; gene; ss.  
 OS  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 PD 31-JAN-2002.  
 PD 29-JUN-2001; 2001WO-US021066.  
 PF 20-JUL-2000; 2000US-0219556P.  
 PR

PR 25-JUL-2000; 2000US-0220585P.  
 PR 25-JUL-2000; 2000US-0220605P.  
 PR 25-JUL-2000; 2000US-0220607P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220638P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 25-JUL-2000; 2000US-0220666P.  
 PR 26-JUL-2000; 2000US-0220693P.  
 PR 28-JUL-2000; 2000US-0220710P.  
 PR 01-AUG-2000; 2000US-0222425P.  
 PR 22-AUG-2000; 2000US-0227133P.  
 PR 23-AUG-2000; 2000US-0227352P.  
 PR 24-AUG-2000; 2000US-0227332P.  
 PR 10-NOV-2000; 2000US-030873.  
 PR 28-NOV-2000; 2000US-0253646P.  
 PR 01-DEC-2000; 2000US-0303267P.  
 PR 20-DEC-2000; 2000US-0074725P.  
 PR 28-FEB-2001; 2000US-0304956P.  
 PR 01-MAR-2001; 2001US-0006666P.  
 PR 22-MAR-2001; 2001US-0081674P.  
 PR 10-MAY-2001; 2001US-0085420P.  
 PR 15-MAY-2001; 2001US-0085428P.  
 PR 25-MAY-2001; 2001US-0085428P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
 XX P1 Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
 XX WPI: 2002-1172001/22.  
 XX P-PSDB: MAU83658.  
 DR  
 XX  
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumors such  
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
 PT or liver tumor.  
 XX  
 XX  
 XX Claim 2; Fig 133; 359pp; English.  
 XX  
 XX The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
 CC liver tumor. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO  
 CC protein coding sequences of the invention  
 CC  
 XX  
 XX Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
 SQ  
 Query Match 98.6%; Score 2783.4; DB 6; Length 3819;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
 QY 4 CAGCAGGCTCTGCTCTGTCACAGAGGCTGAGGTCAGAGGTCGATCTTGGCTCATGCT 63  
 Db 55 CTGAGAGGCTCTGCTCTGTCACAGAGGCTGAGGTCAGAGGTCGATCTTGGCTCATGCT 114  
 QY 64 AACCTCCACCTCCCGGGTTCAGAGTATCTCACTGCTCAGCTCCCGAGTACCTGGGATT 123  
 Db 115 AACCTCCACCTCCCGGGTTCAGAGTATCTCACTGCTCAGCTCCCGAGTACCTGGGATT 174  
 QY 124 ACAGGTGTGACTTCCAGAGTCACTCCGTGCGAGGAAATATGATCTCCCGAGTCCGCTGCTG 183

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Db 1075 CTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1134  
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Db 1135 CTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1194  
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Db 1195 CCGGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1254  
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Qy 1864 CTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1923  
Db 1915 CTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1974  
Qy 1924 ATCTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1983  
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Qy 2104 TCCGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2163  
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Qy 2284 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2343  
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Db 235 CAGACGACACTGTTCTGCTGAGTCTGTCTTCTGCTGCTCAAGGTCACGAGGAGG 294  
Qy 244 CACAGGAGAGCTTTGCTTCTGCAAGGAGGAAACAGAGACACAGAGAGAGCTTCAC 303  
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Qy 544 AGCTGAGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 603  
Db 595 AGCTGAGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654  
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Qy 784 CAGTTCCTGAAGCATCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843  
Db 835 CAGTTCCTGAAGCATCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 894  
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Qy 904 GACCTGCAATCCCTCCGAG 963  
Db 955 GACCTGCAATCCCTCCGAG 1014  
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Db 1075 CTCTCTCTGAGAGCTTCAG 1134  
Qy 1084 CTGAGTGAAGAGTCTTGGAGAGTGTGTGAACAGAACTCAAGAGAGAGAGAGAGAGAGAG 1143  
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Qy 1324 CTGATGATCTCTGAG 1383  
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Db 2215 GAGCCCTCTCTTGAAG 2274  
Qy 2224 ACTCTGTCAG 2283  
Db 2275 ACTCTGTCAG 2334  
Qy 2284 GGCCTGTCAG 2343  
Db 2335 GGCCTGTCAG 2394  
Qy 2344 CAGACTTTGAAG 2403  
Db 2395 CAGACTTTGAAG 2454









XX Ahenkazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Geber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Kijavini LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI: 2003-328860/31.  
 DR P-PSDB; AB072273.  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides, designated  
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
 PT cancer.  
 PS  
 PS Claim 2; Fig 203; 453pp; English.  
 CC  
 CC The invention describes an isolated nucleic acid (1) comprising, or which  
 CC is at least 80 % sequence identity to, or the full-length coding sequence  
 CC of, any of 118 300-2100 nucleotide sequences, which encodes its  
 CC corresponding PRO polypeptide selected from 118 100-700 amino acid  
 CC sequences, all given in the specification. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS, cancer, or diabetic complications. The nucleic  
 CC acids are useful as hybridization probes, in chromosome and gene mapping,  
 CC and in generating antisense RNA or DNA. The polypeptides are useful as  
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful  
 CC in tissue typing. This sequence encodes a novel human secreted and  
 CC transmembrane PRO polypeptide  
 CC  
 XX  
 SQ Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
 Query Match 98.6%; Score 2783.4; DB 8; Length 3819;  
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;  
 Matches 2810; Conservative 0;  
 QY 4 CAGCAGGCTCTGCTCTGTCACACAGGCTGAGTGAATCTTGGCTCATCTG 63  
 Db 55 CTGAGAGGCTCTGCTCTGTCACACAGGCTGAGTGAATCTTGGCTCATCTG 114  
 QY 64 AACCTCCACCTCCCGGGTCAAGTATTTCTCATGCTCTCCGAGTATGGGATT 123  
 Db 115 AACCTCCACCTCCCGGGTCAAGTATTTCTCATGCTCTCCGAGTATGGGATT 174  
 QY 124 ACAGGTGATGATCTTCAAGAGTACTCCGTCGAGAAATGACTCCGAGTGGCTG 183  
 Db 175 ACAGGTGATGATCTTCAAGAGTACTCCGTCGAGAAATGACTCCGAGTGGCTG 234  
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 Db 415 CATGCCCTTTCCCTGCAAGCCACCTGCTTCCGATCTTCCCTGACCCCAAGGAGCT 474  
 QY 424 TACCACTTCTGCTCTCACTGGAACCAAGATGAGGAGATTAATCTTCTTATGGAG 483  
 Db 475 TACCACTTCTGCTCTCACTGGAACCAAGATGAGGAGATTAATCTTCTTATGGAG 534  
 QY 484 CTGAGCTTCTTGTGATGACCAAGCTCTAGCTCTCTCTTCAAGACCAAGAGAG 543  
 Db 535 CTGAGCTTCTTGTGATGACCAAGCTCTAGCTCTCTCTTCAAGACCAAGAGAG 594

QY 544 AGCTTGCTCAGAGGCCCCCGCTTTAGCACTTCTGTCACCTCTGAGGAGCTTCAG 603  
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 QY 604 AACATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663  
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Db 1915 CTGGGACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1974
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Db 2813 CTGGCGAGAGAGAGGCGCTTTGCCAGAGCAAGAGAGAGCTCGCTTACCTTGAAGCC 2871

RESULT 15
ACAO3805
ID ACAA03805 standard; cDNA, 3819 BP.
XX
AC ACAA03805;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #203.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumor necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW 88.
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 28-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
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06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUN-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 18-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001US-00908827.  
PR 18-JUL-2001; 2001US-00924419.  
PR 06-AUG-2001; 2001US-00927796.  
PR 09-AUG-2001; 2001US-00931836.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Garilisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
XX  
XX WPI; 2003-333040/31.  
XX P-PSDB; ABU66772.  
XX  
XX New secreted and transmembrane PRO nucleic acids, useful for gene  
XX therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
XX typing, and in chromosome identification.  
XX  
XX Claim 2; Fig 405; 660pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The PRO polypeptides are useful for  
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
CC human blood, for stimulating the proliferation or differentiation of  
CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
CC in chromosome and gene mapping, in the generation of antisense RNA and  
CC DNA, in the preparation of PRO polypeptides, for generating transgenic  
CC animals or knockout animals, for the genetic analysis of individuals with  
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
CC encoding the human PRO polypeptides of the invention. Note: The sequence  
CC data for this patent was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/patidbidentity.html](http://seqdata.uspto.gov/patidbidentity.html)  
XX  
XX Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
SQ  
Query Match 98.6%; Score 2783.4; DB 8; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
QY 4 CAGCAGGCTCTGCTGTCACACAGGCTGAGTGAAGTGTGATCTTGGCTCATCGT 63  
DB CTGAGAGGCTCTGCTGTCACACAGGCTGAGTGAAGTGTGATCTTGGCTCATCGT 114  
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Search completed: February 12, 2005, 10:48:32  
Job time : 1485 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:22:24 ; Search time 469 Seconds  
(without alignments)  
9845.571 Million cell updates/sec

Title: US-10-073-054-1

Perfect score: 2822  
Sequence: 1 cgcgcagcagcggctcgcctc.....ctgcctcctcgcgcgcg 2822Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapect 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2075.8	73.6	3090	US-09-276-531-78	Sequence 78, Appl
2	554.4	19.6	556	US-09-262-537-45	Sequence 45, Appl
3	215	7.6	356	US-09-513-999C-12063	Sequence 12063, A
4	205.2	7.3	354	US-09-621-976-10391	Sequence 10391, A
5	115.4	4.1	1651	US-09-484-970B-17	Sequence 17, Appl
6	111	3.9	3453	US-09-949-016-12256	Sequence 12256, A
7	111	3.9	34540	US-09-949-016-13156	Sequence 13156, A
8	111	3.9	45546	US-09-146-053-6	Sequence 6, Appl
9	110.6	3.9	393753	US-09-949-016-14573	Sequence 14573, A
10	110.6	3.9	393753	US-09-949-016-14574	Sequence 14574, A
11	110.6	3.9	818128	US-09-949-016-14546	Sequence 14546, A
12	110.6	3.9	818128	US-09-949-016-14547	Sequence 14547, A
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43	108.6	3.8	52865	US-09-949-016-15618	Sequence 15618, A
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45	108.6	3.8	86213	US-09-949-016-17240	Sequence 17240, A

## ALIGNMENTS

RESULT 1  
US-09-276-531-78  
Sequence 78, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: yue, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

RECEPORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION NUMBER: 42,918

REFERENCE/DOCKET NUMBER: PA-0008 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 3090 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRAINOT14



CLONE: 1595762  
US-09-276-531-78

Query Match 73.6%; Score 2075.8; DB 3; Length 3090;  
Best Local Similarity 99.1%; Fred. No. 0;  
Matches 2139; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

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## RESULT 2

US-09-262-537-45  
Sequence 45, Application US/09262537  
Patent No. 6479256  
GENERAL INFORMATION:  
APPLICANT: Hayflick, Joel  
TITLE OF INVENTION: Lectomedin Materials and Methods  
FILE REFERENCE: 2786/35307  
CURRENT FILING DATE: 1999-03-04  
PRIOR FILING DATE: 1998-03-04  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 45  
LENGTH: 556  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-262-537-45

Query Match 19.6%; Score 554.4; DB 4; Length 556;  
Best Local Similarity 99.8%; Pred. No. 6,7e-118;  
Matches 555; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1879 ACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1938  
Db 301 ACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
QY 1939 GTGGTGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1998  
Db 361 GTGGTGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 1999 CTGGGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2058  
Db 421 CTGGGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 2059 GGCACCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2118  
Db 481 GGCACCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 2119 CTCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2134  
Db 541 CTCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556

RESULT 3  
US-09-513-999C-12063

Sequence 12063, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59,US2,REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 12063  
LENGTH: 356  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 103  
OTHER INFORMATION: s=g or c  
US-09-513-999C-12063

Query Match 7.6%; Score 215; DB 4; Length 356;  
Best Local Similarity 100.0%; Pred. No. 5.1e-40;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 67  
Db 142 AGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201  
QY 68 TCCACCTCCCGGCTTCAAGTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 127  
Db 202 TCCACCTCCCGGCTTCAAGTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261  
QY 128 GTGGTGCATTCAGAGAGTATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187  
Db 262 GTGGTGCATTCAGAGAGTATCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321  
QY 188 CGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 222  
Db 322 CGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 356

## RESULT 4

US-09-621-976-10391/C  
Sequence 10391, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jober, S.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054PR2  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 10391  
LENGTH: 354  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 195,280,300  
OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-10391

Query Match 7.3%; Score 205.2; DB 4; Length 354;  
Best Local Similarity 96.4%; Pred. No. 9e-38;  
Matches 240; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY 1867 GTGACGTACATACCAACCTGGGCTCTTCAAGCTT-GGTTTCTGTTCACATGGCCAT 1925  
DB 354 GTGACGTACATACCAACCTGGGCTCTTCAAGCTTGGTTTCTGTTCACATGGCCAT 295  
QY 1926 GCTTGGCCATGTTGGTGGAGATCTTGGGGCTGGGCCCCCAGACCCAAAGTGTGACA 1985  
DB 294 GCTAG-CACCATGTGTTGGTGGAGATCTT-TGGCTGGCCCCCAGACCCAAAGTGTGACA 237  
QY 1986 TGTGCTGACATGCTGGGCTCTGAGCTGTGCTTGGGCTGGGCTGGGCTGTGATCTTCT 2045  
DB 236 TGTGCTGACATGCTGGGCTCTGAGCTGTGCTTGGGCTGGGCTGGGCTGTGATCTTCT 177  
QY 2046 CTCTTTGCTTCTGGGCTCTTCAAGCTTGTGCTTCACTTTTCAAGATCATCACTTC 2105  
DB 176 CTCTTTGCTTCTGGGCTCTTCAAGCTTGTGCTTCACTTTTCAAGATCATCACTTC 117  
QY 2106 CTTCAGAG 2114  
DB 116 CTTCAGAG 108

## RESULT 5

US-09-484-970B-17  
Sequence 17, Application US/09484970B  
Patent No. 6426186  
GENERAL INFORMATION:  
APPLICANT: Jones, Karen A.  
APPLICANT: Volkmueth, Wayne  
APPLICANT: Walker, Michael G.  
TITLE OF INVENTION: BONE REMODELING GENES  
FILE REFERENCE: PB-0014 US  
CURRENT APPLICATION NUMBER: US/09/484,970B  
CURRENT FILING DATE: 2000-01-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PERL Program  
SEQ ID NO 17  
LENGTH: 1651  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6426186 126510.2CB1  
NAME/KEY: unsure  
LOCATION: 767-846  
OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-17

Query Match 4.1%; Score 115.4; DB 3; Length 1651;

Best Local Similarity 51.3%; Pred. No. 6.9e-17; Matches 337; Conservative 0; Mismatches 296; Indels 24; Gaps 2;

QY 1492 AAGGTGACATGAACTGCTGTGAGCCGCTTCTGCTGAGACAGAGCTTCTGTGAGC 1551  
DB 5 AAGATTCACGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 64  
QY 1552 GAGCCGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1611  
DB 65 GTGGGAGGTGGTCAAGGGGCTGATGTGCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 124  
QY 1612 TTCTCCCTGCTACCTGCTTCTTCTGATGGGCTTCAAGGGGCTTCAAGGGGCTTCAAGGGGCT 1671  
DB 125 TACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184  
QY 1672 GTGTGAGAGGTCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1731  
DB 185 GCTGTCAAGGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 244  
QY 1732 TGGGGCTTCCCATCTTCTTCTGATGAGCTGATGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1791  
DB 245 TGGGGCTGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 304  
QY 1792 CCCATCATCTTGTGCTGTGATGAGACTCCAGAGGGGCTCATCTA-----CCCT 1839

DB 305 ACCATTCGTATGAGGAGAACCCGACCTCTTGAAGCTATGCTGCTCCGTGAAGAGACA 364  
QY 1840 TCCATGTGCTGATATCCGGGACTCCCTGTGCTACATACCAACCTGGGCTCTTCAAGC 1899  
DB 365 ACCATGTATGCGCTCTATATATACCGGTCAACGGGTACTTCTCATACCTTCTCTTGGC 424  
QY 1900 CTGTGTTCTTCTTCAACATGAGCCATGATGATGATGATGATGATGATGATGATGATGATG 1959  
DB 425 ATGTGTGCTGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484  
QY 1960 CGCCCCACACCCAAAGTGTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2019  
DB 485 AAGAGCGGGGAGAGAACCGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544  
QY 2020 GAGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2079  
DB 545 GGTGTGATGAGGGGGTGGCCATCTTCAAC-----CCGTTGGGCTCTTCACAC 592  
QY 2080 CTCTACCTTTCAGATCATGACCTCTTCAAGGCTTCTCATCTTGTATGCTGATG 2136  
DB 593 GTTACATCTTGTGACCTTTCACCTTGTGAGAGGTGCTTCACTGCTGCTGCTGCTGCTGCTG 649

## RESULT 6

US-09-949-016-12226/C  
Sequence 12226, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12226  
LENGTH: 34539  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12226

Query Match 3.9%; Score 111; DB 4; Length 34539;

Best Local Similarity 86.0%; Pred. No. 2.3e-15; Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 7 CAGGCTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66  
DB 27949 CAGATTCGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 27890  
QY 67 CTTCACCTCCCGGGTTCAGATGATCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126  
DB 27889 CTTCACCTCCCGGGTTCAGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 27830  
QY 127 GGTGTGACTTTCAGAGTACT 149  
DB 27829 GGCACACTACACGCGCTGCT 27807

## RESULT 7

US-09-949-016-13156/C  
Sequence 13156, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13156  
LENGTH: 34540  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-13156

Query Match 3.9%; Score 111; DB 4; Length 34540;  
Best Local Similarity 86.0%; Pred. No. 2.3e-15;  
Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

7 CAGGCTCTGCTCTGTCAACAGGCTGAGTGTGATCTTGCTCATGTAC 66  
DB 27949 CAGATTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGCTCATCGCAC 27890  
QY 67 CTCACCTCCCGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGATTACA 126  
DB 27889 CTCACCTCCCGGTTCAAGTATCTCTGCTCAGCTCCCGAGTACGGATTACA 27830  
QY 127 GGTGTGACTTCCAGAGTACT 149  
DB 27829 GGCACACTACCAAGCCTGGCT 27807

RESULT 8  
US-09-146-053-6/c

Sequence 6, Application US/09146053A  
Patent No. 639349  
GENERAL INFORMATION:  
APPLICANT: Ryan, James W.  
APPLICANT: Sprinkle, Terry Joe Curtis  
APPLICANT: Venema, Richard C.  
TITLE OF INVENTION: Human Aminopeptidase P Gene  
FILE REFERENCE: MCG103  
CURRENT APPLICATION NUMBER: US/09/146,053A  
CURRENT FILING DATE: 1998-09-02  
EARLIER APPLICATION NUMBER: 60/057,854  
EARLIER FILING DATE: 1997-09-02  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 6  
LENGTH: 45546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-146-053-6

Query Match 3.9%; Score 111; DB 3; Length 45546;  
Best Local Similarity 86.0%; Pred. No. 2.5e-15;  
Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

7 CAGGCTCTGCTCTGTCAACAGGCTGAGTGTGATCTTGCTCATGTAC 66  
DB 25748 CAGATTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGCTCATCGCAC 25689  
QY 67 CTCACCTCCCGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGATTACA 126  
DB 25688 CTCACCTCCCGGTTCAAGTATCTTGCTCAGCTCCCGAGTACGGATTACA 25629  
QY 127 GGTGTGACTTCCAGAGTACT 149  
DB 25628 GGCACACTACCAAGCCTGGCT 25606

RESULT 9  
US-09-949-016-14573  
Sequence 14573, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14573  
LENGTH: 393753  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(393753)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14573

Query Match 3.9%; Score 110.6; DB 4; Length 393753;  
Best Local Similarity 86.5%; Pred. No. 7.2e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

9 GGGTCTGCTCTGTCAACAGGCTGAGTGTGATCTTGCTCATGTAC 68  
DB 145223 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGCTCATGTAC 145282  
QY 69 CCACCTCCCGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGATTACA 128  
DB 145283 CCACCTCCCGGTTCAAGTATCTCTGCTCAGCTCCCGAGTACGGATTACA 145342  
QY 129 TGGTGAATCCAGAGTACT 149  
DB 145343 CGCCCGCACACGCTGGCT 145363

RESULT 10

US-09-949-016-14574  
Sequence 14574, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14574  
LENGTH: 393753  
TYPE: DNA  
ORGANISM: Human

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(393753)

OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14574

Query Match 3.9%; Score 110.6; DB 4; Length 391753;  
Best Local Similarity 86.5%; Pred. No. 7.2e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 68  
DB 145223 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 145282  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 128  
DB 145283 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 145342  
QY 129 TGGTACTTCCAGAGTACT 149  
DB 145343 CGCCCGCACACAGCCTGGCT 145363

RESULT 11  
US-09-949-016-14546

Sequence 14546, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14546  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14546

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 68  
DB 569598 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 569657  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 128  
DB 569658 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 569717  
QY 129 TGGTACTTCCAGAGTACT 149  
DB 569718 CGCCCGCACACAGCCTGGCT 569738

RESULT 12

US-09-949-016-14547  
Sequence 14547, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14547  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14547

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 68  
DB 569598 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 569657  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 128  
DB 569658 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCCTCCGAGTAGCTGGGATTACAG 569717  
QY 129 TGGTACTTCCAGAGTACT 149  
DB 569718 CGCCCGCACACAGCCTGGCT 569738

RESULT 13

US-09-949-016-14548  
Sequence 14548, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14548  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14548

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTACACAGAGCTGAGTGCAGTGTGATCTTGGCTCATCGTAACCT 68

Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTCGGCTCACTCAACT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 569717  
Qy 129 TGTGACTTCCAGAGTACT 149  
Db 569718 CGCCCGCACACCGCTGGCT 569738

## RESULT 14

US-09-949-016-14549  
; Sequence 14549, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14549  
; LENGTH: 818128  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(818128)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14549

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 9 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGGCTCATGTAACCT 68  
Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGGCTCATGTAACCT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 569717  
Qy 129 TGTGACTTCCAGAGTACT 149  
Db 569718 CGCCCGCACACCGCTGGCT 569738

## RESULT 15

US-09-949-016-14550  
; Sequence 14550, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14550  
; LENGTH: 818128  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(818128)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14550

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 9 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGGCTCATGTAACCT 68  
Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTTGGCTCATGTAACCT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGGATTACAG 569717  
Qy 129 TGTGACTTCCAGAGTACT 149  
Db 569718 CGCCCGCACACCGCTGGCT 569738

Search completed: February 12, 2005, 16:47:38  
Job time : 485 secs



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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:23:49 / Search time 1542 Seconds  
(Without alignments)  
10798.377 Million cell updates/sec

Title: US-10-073-054-1

Perfect score: 2822  
Sequence: 1 CGGAGCAGGAGGCTGCTCTC.....CTGGCCTACCTCTGAGCCG 2822

Scoring table:  
IDENTITY/NUC  
Gap 10.0, Gapext 1.0

Searched: 5378673 seqs, 295022984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2822	100.0	2822	9 US-09-845-771-1	Sequence 1, Appl
2	2822	100.0	2822	15 US-10-225-567A-517	Sequence 517, App
3	2822	100.0	2822	16 US-10-073-054-1	Sequence 1, Appl
4	2822	100.0	2822	17 US-10-460-479-1	Sequence 767, App
5	2820	99.9	2821	17 US-10-295-027-767	Sequence 20017, A
6	2785.4	98.7	3902	10 US-09-814-353-20017	Sequence 482, App
7	2783.4	98.6	3819	9 US-09-978-295A-482	Sequence 482, App
8	2783.4	98.6	3819	9 US-09-978-697-482	Sequence 482, App
9	2783.4	98.6	3819	9 US-09-978-192A-482	Sequence 482, App
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#### ALIGNMENTS

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US-09-845-771-1  
Sequence 1, Application US/09845771  
Publication No. US20020040132A1  
GENERAL INFORMATION:  
APPLICANT: Brennard, John  
TITLE OF INVENTION: Methods  
FILE REFERENCE: 1991-197  
CURRENT APPLICATION NUMBER: US/09/845, 771  
CURRENT FILING DATE: 2001-05-02  
PRIORITY APPLICATION NUMBER: 60/201, 422  
PRIORITY FILING DATE: 2000-05-03  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 2822  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-845-771-1  
Query Match 100.0%; Score 2822; DB 9; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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US-10-073-054-1  
Sequence 1, Application US/10073054  
Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding gene  
FILE REFERENCE: 1871-132 (93702-CIP/WRO)  
CURRENT APPLICATION NUMBER: US/10/073,054  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: US 09/308,696  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2822  
TYPE: DNA  
ORGANISM: Human GPR56-1 (TSR32)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (163)..(2241)  
OTHER INFORMATION:  
US-10-073-054-1

Query Match 100.0%; Score 2822; DB 16; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ATTAAGAGTGTGATCTTCAAGAGTGA CTCCTGCTGAGAGAAATGATCTCCCGAGTGG 180  
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QY 181 CTGACAGAGCACTGTTCTGCTGAGTGTGCTCTTCTGCTGCTCAAGGTTGCCACGAGAG 240  
DB 181 CTGACAGAGCACTGTTCTGCTGAGTGTGCTCTTCTGCTGCTCAAGGTTGCCACGAGAG 240  
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DB 1741 CCGATCTTCTGAG 1800  
QY 1801 TTGGCTGAGTGAAG 1860  
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Db 2281 TGGGCTCTGTCAGCACTGCTGTGGCCCCGAGCCAGGCGCCAGCCCAAGTCAG 2340  
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Qy 2461 ACGGAGCTCAGAGATGGCGCCCATGCTGCTTGAAGGTACTGTCCCATCTGTCCCAAC 2520  
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Qy 2821 CG 2822  
Db 2821 CG 2822

RESULT 4  
US-10-460-479-1  
; Sequence 1, Application US/10460479  
; Publication No. US20040093627A1  
; GENERAL INFORMATION:  
; APPLICANT: Brennam, John Charles  
; APPLICANT: Hart, Kevin Anthony  
; TITLE OF INVENTION: Methods GPR56  
; FILE REFERENCE: 1991-220  
; CURRENT APPLICATION NUMBER: US/10/460,479  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: 09/845,771  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,422  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 2822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-460-479-1

Query Match 100.0%; Score 2822; DB 17; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 361 GTCCATGCCCCCTTCCCTGAGAGCCCACTGCTTCCGATCTTCCCTGAGCCGAGG 420  
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2821 CG 2822

RESULT 5  
US-10-295-027-767  
Sequence 767, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glyme, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394





DB 784 AGCGGACCTTCTGAGTGAACAAGCCTTAGCCTCTGCTTCCAGCACAGAGG 843  
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QY 722 GCGAATTCCTGAAAGATCCCGAAGGCTCAAGAGGCTCTGAGTGCCTCCGCGAGCC 781  
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DB 2524 GCACTGTGAG 2583  
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Qy 2821 C 2821  
Db 3122 C 3122

RESULT 7  
US-09-978-295A-482  
Sequence 482, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boetsch, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerder, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700

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37 PRIOR FILING DATE: 1998-05-07
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39 PRIOR FILING DATE: 1998-05-07
40 PRIOR APPLICATION NUMBER: 60/084640
41 PRIOR FILING DATE: 1998-05-07
42 PRIOR APPLICATION NUMBER: 60/084598
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47 PRIOR FILING DATE: 1998-05-07
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55 PRIOR FILING DATE: 1998-05-13
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65 PRIOR FILING DATE: 1998-05-15
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67 PRIOR FILING DATE: 1998-05-15
68 PRIOR APPLICATION NUMBER: 60/085704
69 PRIOR FILING DATE: 1998-05-15
70 PRIOR APPLICATION NUMBER: 60/085697

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Db	115	AACCTCACCTCCGGGTTCA	GTATCTCATGCTCAGCTCCCGAGTACTGGATT	174						
QY	124	ACAGTGTGATCTCCAGAGTGA	CTCCGTGGAGGAAATGATCTCCCATGCTGTCTG	183						
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QY	184	CAGACGACATGTTTCTGTG	AGTCTGCTTCTGTGTCAGAGTGCACCGGAGGGG	243						
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QY	244	CACAGGGAAGACTTTCGCTT	CTGACAGCCAGCCGAAACAGACACAGAGACGCTTCAC	303						
Db	295	CACAGGGAAGACTTTCGCTT	CTGACAGCCAGCCGAAACAGACACAGAGACGCTTCAC	354						
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Db	355	TACAAACCCACACACGAC	CTGGCGCATCTCATTGAAATCTCCGAAAGAGCCCTCAAGTC	414						
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Db	415	CATGCCCTTTCCTCGAGCC	CACTGCTTCCCGATTCCTTCCCTGACCCAGGGGCTTC	474						
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QY	544	AGCCTGAGCTAGGGCCCC	CCGCTGTATGACCATTTCTGTCACTTCCTGTGTGAGCCTTCAG	603						
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Db	775	CAGTTTCTGAAAGCATCCC	CAGAGGCTCAAGAGGCTCTGGCTGCCCCCGACGACG	834						
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QY	844	TTTCAGAGAGACCGGATAT	CAGCCATGTATGAAAGCTCCAGCCCAAGCCGCGCTTCAG	903						
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Db	1135	CTGGGTGAGAGAGGTCTTTGGGGAATTGGTGTACAGAACACCAAGTATGCCAAGCTCAAGGAG	1194
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Db	2155	TCTTTCAAGAGGCTCTCTCATCTTCACTGTATGTGTATCTGAGCTGAGGCTCGAGGCT	2214

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Db	2335	GGCCTCGTGCACACTGCTGTGTGCCCCGAGGCCCAAGGCCCAAGGCCCAAGTCAACCG	2394
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RESULT 8  
US-09-978-697-462  
Sequence 462, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Akhennazi, Avi  
APPLICANT: Baker Kevin P.  
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APPLICANT: Flvayroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimeldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophie S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR APPLICATION NUMBER: 60/084598



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Sequence 482, Application US/0978192A  
Patent No. US2002017553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 9; Length 3819;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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 DB 55 CTGAGGGCTCTCCCTCTGTGTACACAGGCTGAGTGCAGTGTGATCTTGGCTCATCGT 114  
 QY 64 AACCTTCACCTCCCGGTTCAAGTATTCATGCTCAGCTCCGAGTAGTGGATT 123  
 DB 115 AACCTTCACCTCCCGGTTCAAGTATTCATGCTCAGCTCCGAGTAGTGGATT 174  
 QY 124 ACAGGTGTGATCTTCAAGAGTGACTCGTGGAGAAATGACTCCCACTCGCTGTG 183

Db	175	ACAGGAGGTACATTCCAAAGATGATCTCGTGGAGGAAATATGATCTCCAGATGAGTCTG	234
Qy	184	CAGACGACACTGTTCTCTGATGAGTCTGCTTTCTGATCCAAAGTCCACACGGCAGGGCC	243
Db	235	CAGACGACACTGTTCTCTGATGAGTCTGCTTTCTGATCCAAAGTCCACACGGCAGGGCC	294
Qy	244	CACAGGGGAACATTTCCGCTTCTGACGACACGGGAACACGACACACAGAGACAGCTTCCAC	303
Db	295	CACAGGGGAACATTTCCGCTTCTGACGACACGGGAACACGACACACAGAGACAGCTTCCAC	354
Qy	304	TACAAACCCACACCAAGACCTGCGCATCTCCATGAGAACCTCCGAAAGAGGCTTCACAGTCC	363
Db	355	TACAAACCCACACCAAGACCTGCGCATCTCCATGAGAACCTCCGAAAGAGGCTTCACAGTCC	414
Qy	364	CATGCCCCCTTCCCTGCAAGCCCACTCTGCTTCCCGATCTTCCCTGACCCCAAGGGCTTC	423
Db	415	CATGCCCCCTTCCCTGCAAGCCCACTCTGCTTCCCGATCTTCCCTGACCCCAAGGGCTTC	474
Qy	424	TACACATTTCCGCTCTACTGGAACCGACATGCTGGAGAGATTACATCTTCTCTATGGCAAG	483
Db	475	TACACATTTCCGCTCTACTGGAACCGACATGCTGGAGAGATTACATCTTCTCTATGGCAAG	534
Qy	484	CGTACATTTCTTGTGATGATGACAAAGCCTCTAGCTCTCTGCTTCCAGACACAGAGAG	543
Db	535	CGTACATTTCTTGTGATGATGACAAAGCCTCTAGCTCTCTGCTTCCAGACACAGAGAG	594
Qy	544	AGCTTGAGTCAAGGGCCCCCGCTGTATAGCACTTCTGTACCTCTGCTGTGAAGCCCTCAG	603
Db	595	AGCTTGAGTCAAGGGCCCCCGCTGTATAGCACTTCTGTACCTCTGCTGTGAAGCCCTCAG	654
Qy	604	AACATCAGCCCTGCCACAGTGCAGCCAGGCTTCACTTCTCTTCCACAGTCTCTCCACACG	663
Db	655	AACATCAGCCCTGCCACAGTGCAGCCAGGCTTCACTTCTCTTCCACAGTCTCTCCACACG	714
Qy	664	GCCGCTCACATATGCTCTGATGAGACATATGATGAGAGCTCAAAAGGAGCTTCCAGCTGTACG	723
Db	715	GCCGCTCACATATGCTCTGATGAGACATATGATGAGAGCTCAAAAGGAGCTTCCAGCTGTACG	774
Qy	724	CAGTTCTCGAAGCATCCCAAGAGGCTCAAGAGAGGCTCTGAGCTGCCCCGACAGCAG	783
Db	775	CAGTTCTCGAAGCATCCCAAGAGGCTCAAGAGAGGCTCTGAGCTGCCCCGACAGCAG	834
Qy	784	CAGTTGCAAGACCTTGAGATGCAAACTGACTCTGTGAGATTCAATGGGGAACATGTGTCC	843
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Qy	844	TTTCAAGAGAGACCCGATCAAGCCACGGTATGAAAGCTCAAGGCCCAACAGCCGAGCTCAG	903
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Qy	904	GACCTGCAATCTCACTCCCGCAGAGAGAGAGCAAGACGAATCATGAGTACTTGGGTG	963
Db	955	GACCTGCAATCTCACTCCCGCAGAGAGAGAGCAAGACGAATCATGAGTACTTGGGTG	1014
Qy	964	CTGCTGCTTCCAAACTTTTCCAGAGGACGAAAGCCGAGACCGGAGAGGCTGGAAGAAGA	1023
Db	1015	CTGCTGCTTCCAAACTTTTCCAGAGGACGAAAGCCGAGACCGGAGAGGCTGGAAGAAGA	1074
Qy	1024	CTTCTCTGATGACCTTCAAGACGCAACCCCTGTTCACAGACAAGATTTCCAGCCAAATC	1083
Db	1075	CTTCTCTGATGACCTTCAAGACGCAACCCCTGTTCACAGACAAGATTTCCAGCCAAATC	1134
Qy	1084	CTGGGTGAGAAAGTCTTGGGGATTTGTGTACAGAACACCAAAATGATCCAACTCACGGAG	1143
Db	1135	CTGGGTGAGAAAGTCTTGGGGATTTGTGTACAGAACACCAAAATGATCCAACTCACGGAG	1194
Qy	1144	CCCGTGTGTCTCACTTTCACAGACCAAGCTACAGCCGAGAGAAATGTGTACTCTCAATGTGTG	1203
Db	1195	CCCGTGTGTCTCACTTTCACAGACCAAGCTACAGCCGAGAGAAATGTGTACTCTCAATGTGTG	1254
Qy	1204	TTCTGGGTGAAAGCCCAATTTGACAGCCCGGGGCAATTGGAGCATGTCTGGGTGTAG	1263

Db	1255	TTCTGGGTTGAAGAACCCCACTTTGAGCAGCCCGGAGCATTTGAGAGTGGCTGGGTGTGAG	1314
Oy	1264	ACCGTCAGAGAGAGAAACCCAAACATCTCTGCTTTCTGCAACCACTTGAACCTTATGCAAGG	1323
Db	1315	ACCGTCAGAGAGAGAAACCCAAACATCTCTCTCTGCAACCACTTGAACCTTATGCAAGG	1374
Oy	1324	CTGATGGTCTCCCTCGGTGAGAGTGAAGCCCGTGCACAAAGCACTACTGAGCCTCTCTCC	1383
Db	1375	CTGATGGTCTCTCTCTCGGTGAGAGTGAAGCCCGTGCACAAAGCACTACTGAGCCTCTCTCC	1434
Oy	1384	TACGTGGAGCTGTGTGCTCTCTGCTCCCTGAGCTGCTTGTCAACATTTGGCCCTAACCTCTCC	1443
Db	1435	TACGTGGAGCTGTGTGCTCTCTGCTCCCTGAGCTGCTTGTCAACATTTGGCCCTAACCTCTCC	1494
Oy	1444	TTCAAGGATGGCCCTGGCCGTGTCAGAGAGAAACCTCGGAGCTAACACATCAAGGTGCATATG	1503
Db	1495	TTCAAGGATGGCCCTGGCCGTGTCAGAGAGAAACCTCGGAGCTAACACATCAAGGTGCATATG	1554
Oy	1504	AACCTGTGTGTGGCCCGTCTTCTGTGTGACACAGAGCTTCTGTGTACAGACCCGTGTGGCC	1563
Db	1555	AACCTGTGTGTGGCCCGTCTTCTGTGTGACACAGAGCTTCTGTGTACAGACCCGTGTGGCC	1614
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Db	1615	CTGACAGGCTCTGAGGCTGGCTGTCCAGACCAAGTGCATCTTCCGTGACATTTCTCCGTGC	1674
Oy	1624	ACCGACCTTTCCTGAGATGGGCTTCGAGAGGGTACAACTCTAACCGACTGTGTGAGAGTCT	1683
Db	1675	ACCGACCTTTCCTGAGATGGGCTTCGAGAGGGTACAACTCTAACCGACTGTGTGAGAGTCT	1734
Oy	1684	TTTGGCACTATATGTCTCTGTGGCTACCTATCACTGACAGGCCCATGGGCTGGGGCTTCCCC	1743
Db	1735	TTTGGCACTATATGTCTCTGTGGCTACCTATCACTGACAGGCCCATGGGCTGGGGCTTCCCC	1794
Oy	1744	ATCTTTCGTGTGAAGCTGTGTGGCCCTGTGTGATGTGACAACTATGGCCCATCATCTTG	1803
Db	1795	ATCTTTCGTGTGAAGCTGTGTGGCCCTGTGTGATGTGACAACTATGGCCCATCATCTTG	1854
Oy	1804	GCTGTGCATAGAGATCTCGAGAGGGCGTATCTACCTTCCATGTGTCTGGAGATCCCGGAGCTCC	1863
Db	1855	GCTGTGCATAGAGATCTCGAGAGGGCGTATCTACCTTCCATGTGTCTGGAGATCCCGGAGCTCC	1914
Oy	1864	CTGTGCAGCTACATCAACCAACTGGGCTCTTACGAGCTGTGTGTCTGTCAACATGGCC	1923
Db	1915	CTGTGCAGCTACATCAACCAACTGGGCTCTTACGAGCTGTGTGTCTGTCAACATGGCC	1974
Oy	1924	ATGTAGGCCAATAGTGTGTGCAGATCTTGCGGCTGCGCCGCCCAACACCCAAAGTGTCTCA	1983
Db	1975	ATGTAGGCCAATAGTGTGTGCAGATCTTGCGGCTGCGCGCCGCCCAACACCCAAAGTGTCTCA	2034
Oy	1984	CATGTGCTGAACATGTGGGGCTCAAGCTGTGCTTGTGGCCGACCTGTGGGCTTGTATCTTC	2043
Db	2035	CATGTGCTGAACATGTGGGGCTCAAGCTGTGCTTGTGGCCGACCTGTGGGCTTGTATCTTC	2094
Oy	2044	TTCTCTTTGGCTTCTGGACACTTCACAGCTTGTGTCTTACCTTTTCAGATCATCAAC	2103
Db	2095	TTCTCTTTGGCTTCTGGACACTTCACAGCTTGTGTCTTACCTTTTCAGATCATCAAC	2154
Oy	2104	TTCTTTCGAAGCTTCTCATCTTATCACTGTGATGTGTCAAGGCGCTGCAGGCCCGGGGT	2163
Db	2155	TTCTTTCGAAGGTTCTCATCTTATCACTGTGATGTGTCAAGGCGCTGCAGGCCCGGGGT	2214
Oy	2164	GGCCCTCTCCCTCTGAGAGACACTCAAGCTGCGCAGAGCTTCCCATAGCTCTCGGCGAGC	2223
Db	2215	GGCCCTCTCCCTCTGAGAGACACTCAAGCTGCGCAGAGCTTCCCATAGCTCTCGGCGAGC	2274
Oy	2224	ACCTGTCTAGGCCGATCTAGGCTCTCAGGCCCACTGCGCATGTGATGAAGCAGAGATGC	2283
Db	2275	ACCTGTCTAGGCCGATCTAGGCTCTCAGGCCCACTGCGCATGTGATGAAGCAGAGATGC	2334
Oy	2284	GGCTGTGTGCACATGTGCTGTGGCCCGGAGCCAGGCCCAAGGCCCAAGCTGTAGCCG	2344
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RESULT 10
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; Sequence 482, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30

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PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 9; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;  
Matches 2810; Conservative 0

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295 CACAGGAGAACTTCTGCTTCTGAGCGAGGAGAAACAGACACAGAGAGACCTCCAC 354  
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CAGTTCTGAGAGCATCCCAAGAGGCTCAAGAGGCTTCCAGGCTCAGCAGCAG 834



APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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QY 64 AACCTCCCTCCGGGTTCAAGTATCTCATGCTCAGCTCCCGAGTAGCTGGATT 123  
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2035 CATGTGTGAGTCACTGTGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2094  
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2275 ACCCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2334  
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2335 GAGCTGTGTGAGCACTGT 2394  
2344 CAGACTTTTGGAAAGCCCAAGCACTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2403  
2395 CAGACTTTTGGAAAGCCCAAGCACTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2454  
2404 CCGGGGCTGTGGGCTTTTGAATTTGAGCTTTGAGGAGTACTGTGAGTCACTGAGTCCAG 2463  
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## RESULT 12

US-09-978-608A-482

Sequence 482, Application US/09978608A  
Publication No. US20030045462A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P26301C22  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File wrapper or Palm  
SEQ ID NO 482  
LENGTH: 3819  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-482

Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
Qy 4 CAGCAGGGCTCTGCTGT 63

Db 55 CTGAGGAGTCTCGCTCTGTCAACAGGCTGAGTGAAGTGTGATCTTGGGCTCATCGT 114  
Qy 64 AACCTCACTCCCGGGTCAAGTATTCATCTCACTCACTCCGAGTATGCTGGGAT 123  
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## RESULT 13

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlt, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 482  
; LENGTH: 3819  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-978-585A-482

Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
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APPLICANT: Kljavin, Ivar J.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: US/09/978,191A  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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55 CTGGAGGCTCTGCTCTGTCACACAGGCTGAGTGCATGCTGATCTTGGCTCATCGT 114  
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Query Match 98.6%; Score 2783.4; DB 10; Length 3819;

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Db	115	AACTTCAACCTCCCGGGTTCAAGTATTTCTATGCTCTACGCTCCGAGTATGCTGGGATT	174
Oy	124	ACAGTGGTGACTTCCAAAGATGATCCGTCCGAGGAGAAATGACTCCCGAGTGCCTGTG	183
Db	175	ACAGTGGTGACTTCCAAAGATGATCCGTCCGAGGAGAAATGACTCCCGAGTGCCTGTG	234
Oy	184	CAGACGACATGTTCTGTGTGAGTCTGCTCTTCTGTGTCCAAAGTGTCCACGGCAGGGGC	243
Db	235	CAGACGACATGTTCTGTGTGAGTCTGCTCTTCTGTGTCCAAAGTGTCCACGGCAGGGGC	294
Oy	244	CACAGGGAGAGCTTCCGCTTCTGTGAGCAGAGGAGAACAGACACACAGAGAGCTTCAC	303
Db	295	CACAGGGAGAGCTTCCGCTTCTGTGAGCAGAGGAGAACAGACACACAGAGAGCTTCAC	354
Oy	304	TACAAACCCAACCAAGACCTGCGCATCTCATTCAGAACTCCGAAAGAGGCTTCACATG	363
Db	355	TACAAACCCAACCAAGACCTGCGCATCTCATTCAGAACTCCGAAAGAGGCTTCACATG	414
Oy	364	CATGCCCCCTTCCCTGCAGGCCACCCGTGCTTCCGATCTTCCCTGATCCCAAGGGGCTC	423
Db	415	CATGCCCCCTTCCCTGCAGGCCACCCGTGCTTCCGATCTTCCCTGATCCCAAGGGGCTC	474
Oy	424	TACCACTTCTGCTCTACTGTGAGCCGACATGCTGGAGATTACATCTTCTCTATGAGCAAG	483
Db	475	TACCACTTCTGCTCTACTGTGAGCCGACATGCTGGAGATTACATCTTCTCTATGAGCAAG	534
Oy	484	CGTAGCTTCTTGTGATGAGCAAAAGCCTTAAAGCTCTTGTGCTTCCAGACACAGAGAGAG	543
Db	535	CGTAGCTTCTTGTGATGAGCAAAAGCCTTAAAGCTCTTGTGCTTCCAGACACAGAGAGAG	594
Oy	544	AGCTTGCTCAAGGGCCCCCGCTGTAAAGCACTTGTGACATCTCTGTGAGAGCCCTCAG	603
Db	595	AGCTTGCTCAAGGGCCCCCGCTGTAAAGCACTTGTGACATCTCTGTGAGAGCCCTCAG	654
Oy	604	AAACATCAGCCCTGCGAGTGCAGCCAGCTTCACTTCTTCCACAGTCTCCCAACAG	663
Db	655	AAACATCAGCCCTGCGAGTGCAGCCAGCTTCACTTCTTCCCAAGTCTCCCAACAG	714
Oy	664	GCCGCTCAAAATGCTCGGTGAGCATGTGCAAGCTCAAAAGGAGCTTCAAGTGTCAAGC	723
Db	715	GCCGCTCAAAATGCTCGGTGAGCATGTGCAAGCTCAAAAGGAGCTTCAAGTGTCAAGC	774
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Oy	784	CAGTTGCAAGCTTGGAGTCCGAACTGACTTGTGTGATTTCAATGGGGGACATGTGTCC	843
Db	835	CAGTTGCAAGCTTGGAGTCCGAACTGACTTGTGTGATTTCAATGGGGGACATGTGTCC	894
Oy	844	TTTCGAGAGAGACCGGATCAAGCCACGGTATGGAAGCTCCAGGCCACAGCCGAGCTCCAG	903
Db	895	TTTCGAGAGAGACCGGATCAAGCCACGGTATGGAAGCTCCAGGCCACAGCCGAGCTCCAG	954
Oy	904	GACCTGCACATCACTCCCGGACAGAGAGAGAGCAGACGAGATCATGAGTATCTCGGTG	963
Db	955	GACCTGCACATCACTCCCGGACAGAGAGAGAGCAGACGAGATCATGAGTATCTCGGTG	1014
Oy	964	CTGCTGCTCCGAACCTCTTCCAGAGAGCAAAAGCCCGAGTGGGAGGCTGTAGAAAGCA	1023

Db	1015	CTGTGTGCTTGAAACACTTTCAGAGAGAGAGAAAGGCGGAGCGGGAGGCTAGAGAGAA	1074
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Db	1075	CTCTCTCTGGTGGACCTTCAGACAGCCAGCCCTGGTTCAGAGACAAAGATTCCAGCCAAATGC	1134
OY	1084	CTGGGTGAGAAAGGTCTTGGGGATTGTGTATCAGAAACCAAGTACCAACTCAGCGAG	1143
Db	1135	CTGGGTGAGAAAGGTCTTGGGGATTGTGTATCAGAAACCAAGTACCAACTCAGCGAG	1194
OY	1144	CCCGTGGTGTCACTTTCCAGACACAGCTACAGCCGGAAGAAATGTGACTGTGAAATGTGAG	1203
Db	1195	CCCGTGGTGTCACTTTCCAGACACAGCTACAGCCGGAAGAAATGTGACTGTGAAATGTGAG	1254
OY	1204	TTCTGGGTTTGAAGACCCCAATTGAGCAGCCCGGGGCAATTGAGCAGTGTGGGTGTAG	1263
Db	1255	TTCTGGGTTTGAAGACCCCAATTGAGCAGCCCGGGGCAATTGAGCAGTGTGGGTGTAG	1314
OY	1264	ACCGTCAAGAGAGAAACCCAAACATCTCTGTTCTTGACACATCTTGACCTTATTTGACAGTG	1323
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OY	1324	CTAATGATCTCTCGATGGAGAGGTGAGACGCGGTGCAACAAGCACTACCTGAGCCTCTCTCC	1383
Db	1375	CTAATGATCTCTCGATGGAGAGGTGAGACGCGGTGCAACAAGCACTACCTGAGCCTCTCTCC	1434
OY	1384	TACGTGGAGTGTGTGATCTCTGTCCTGGGCTGCTGCTTGTCAACAATTGCGGCTTACCTTGC	1443
Db	1435	TACGTGGAGTGTGTGATCTCTGTCCTGGGCTGCTGCTTGTCAACAATTGCGGCTTACCTTGC	1494
OY	1444	TTCAGAGGTGCCCCCGCGGTGCAAGAGAGAAACCTCGGAGCTAACACATCAAGATGACATG	1503
Db	1495	TTCAGAGGTGCCCCCGCGGTGCAAGAGAGAAACCTCGGAGCTAACACATCAAGATGACATG	1554
OY	1504	AACCTGTGCTGGCCGCTCTTCTCTGCTGAGACACAGACTTCTGCTCAGACAGCCGGTGGCC	1563
Db	1555	AACCTGTGCTGGCCGCTCTTCTCTGCTGAGACACAGACTTCTGCTCAGACAGCCGGTGGCC	1614
OY	1564	CTGACAGGCTCTGAGGCTGTGGCTGTGCGGAGCCAGTGGCACTTCCCTGAGCTCTCCCTGCTC	1623
Db	1615	CTGACAGGCTCTGAGGCTGTGGCTGTGCGGAGCCAGTGGCACTTCCCTGAGCTCTCCCTGCTC	1674
OY	1624	ACGCGCCCTTTCCTGAGATGAGGCTCGAGAGGGGTCAACCTCTTACCGACTGTGTGTGAGATC	1683
Db	1675	ACGCGCCCTTTCCTGAGATGAGGCTCGAGAGGGGTCAACCTCTTACCGACTGTGTGTGAGATC	1734
OY	1684	TTTGGCACTTATGTCCCTGGCTACTTACTCAAGCTGACGCGCATGTGGCTGGGGCTTTCCCC	1743
Db	1735	TTTGGCACTTATGTCCCTGGCTACTTACTCAAGCTGACGCGCATGTGGCTGGGGCTTTCCCC	1794
OY	1744	ATCTTTCTGTGAGACGCTGTGTGGCCCTGTGTGTGAGATGTGAGCAACTATGAGCCCATCATCTTG	1803
Db	1795	ATCTTTCTGTGAGACGCTGTGTGGCCCTGTGTGTGAGATGTGAGCAACTATGAGCCCATCATCTTG	1854
OY	1804	GCTGTGCAATGAGACTTCAGAGGGGCTCATCTTACCTTTCATGTCTGATTCGGGACTTC	1863
Db	1855	GCTGTGCAATGAGACTTCAGAGGGGCTCATCTTACCTTTCATGTCTGATTCGGGACTTC	1914
OY	1864	CTGGTCAAGCTACATACCAACCTGGGCGCTCTTCCAGCCGATGGTTCTGTCAATGAGCC	1923
Db	1915	CTGGTCAAGCTACATACCAACCTGGGCGCTCTTCCAGCCGATGGTTCTGTCAATGAGCC	1974
OY	1924	ATGTGAGCAACATGATGTGACAGATCTCTGGGCTGTGGCGCCCAACCCAAAGTGTCA	1983
Db	1975	ATGTGAGCAACATGATGTGACAGATCTCTGGGCTGTGGCGCCCAACCCAAAGTGTCA	2034
OY	1984	CATGTGCTGACATCTGCTGGGCTCAGCCTTGGCTCTTGGGCGCGCTGGGCGCTGATCTTC	2043
Db	2035	CATGTGCTGACATCTGCTGGGCTCAGCCTTGGCTCTTGGGCGCGCTGGGCGCTGATCTTC	2094
OY	2044	TTCTCTCTTGGCTCTGGGACCTTCAGACTGTGTGCTCTTCACTTTTCAGATCATCAC	2103
Db	2095	TTCTCTCTTGGCTCTGGGACCTTCAGACTGTGTGCTCTTCACTTTTCAGATCATCAC	2154





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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12008.649 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	1437.4	50.9	3295	3	AK087268 Mus muscu
3	909.6	32.2	966	5	BX381703
4	904	32.0	971	5	BX417949
5	852.6	30.2	941	5	BX384045
6	844.6	29.9	981	5	BX339034
7	843.2	29.9	932	5	BX183659
8	842.8	29.4	965	5	BQ683583
9	829	28.9	870	5	BQ424252
10	816.4	28.9	850	5	BQ146275
11	806.4	28.6	902	5	BQ940423
12	805	28.5	846	6	CA488057
13	803.4	28.5	820	5	BX337534
14	792.6	28.1	877	5	BQ221637
15	792.4	28.1	952	5	BQ678130
16	789.6	28.0	908	5	BQ675934
17	773.8	27.4	917	5	BQ683897
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19	772	27.4	899	5	BQ879177
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21	768.4	27.2	874	4	BG823347
22	758.6	26.9	926	4	BQ677657
23	758.4	26.9	816	4	BG760961
24	755.2	26.8	884	5	BQ232563

25	753.8	26.7	963	5	BQ682600
26	751.6	26.6	1038	4	BM450054
27	748	26.5	847	4	B1257601
28	745.4	26.4	849	4	BG770331
29	740	26.2	859	4	BG818897
30	739.6	26.2	950	5	BQ680533
31	734	26.0	781	4	B1517279
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33	732.2	25.9	799	4	BG818657
34	731.8	25.9	799	6	CD620991
35	729.4	25.8	860	5	BQ877867
36	727	25.8	1112	4	BM452153
37	726.4	25.7	823	2	BF345756
38	723.2	25.6	880	5	BQ778891
39	722.2	25.6	1110	4	BM605296
40	721	25.5	1048	4	BM452235
41	717	25.4	826	5	BQ883069
42	709.4	25.1	817	6	CD246163
43	709.2	25.1	748	4	BM042136
44	703.2	24.9	883	4	B1755503
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## ALIGNMENTS

RESULT 1  
LOCUS BC013207  
DEFINITION Homo sapiens G protein-coupled receptor 56, mRNA (CDNA clone IMAGE:4157209).  
ACCESSION BC013207.1 GI:15301450  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klapper, S.G., Bennett, V., Bennett, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Bueltow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE  
PUBMED  
REFERENCES  
AUTHORS  
TITLE  
JOURNAL

REMARK  
COMMENT  
NIN-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissagel, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAX Plate: 12 Row: e Column: 22  
This clone has the following problem: no 5' EST match.  
Location/Qualifiers

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/lab\_host="DH10B"  
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## ORIGIN

Query Match 97.0%; Score 2737.6; DB 3; Length 3835;  
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Matches 2791; Conservative 0; Mismatches 4; Indels 21; Gaps 3;  
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151 CAGGGTCTCGCTCTGTGACACAGGCTGGAGTGAAGTGTGATCTTGGCTCATCGTAC 210  
67 CTCACCTCCCGGGTCAAGTATTCATGACCTCAAGCTCCGAGTGAAGTGAATTACA 126  
211 CTCACCTCCCGGGTCAAGTATTCATGACCTCAAGCTCCGAGTGAAGTGAATTACA 270  
127 GGTGTGACTTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 186  
271 GGTGTGACTTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 330  
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607 ATGAGCTGCCAGTGGCCGACGTTACCTTCTCTTCAAGTCTTCCCAACAGGAGC 666

DB 751 ATGAGCTGCCAGTGGCCGACGTTACCTTCTCTTCAAGTCTTCCCAACAGGAGC 810  
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Db	1933	GTGATATGGACTCCAGAGGGGGCGCATATACCCCTTCCATGTGCTGAGATCCGGAGCTCCCTG	1992
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Db	1993	GTCACTACATCAACCAACTGTGGGCTCTTCAGCCCTGTGTGTTTCTGTTCAACATGSCATG	2052
Qy	1927	CTAAGCCACATATGTGTGTGACAGATATCTCCGGCTGTGGCCCCCAACCCAAAAGTGTACAT	1986
Db	2053	CTAAGCCACATATGTGTGTGACAGATATCTCCGGCTGTGGCCCCCAACCCAAAAGTGTACAT	2112
Qy	1987	GTGCTGACACTGCTGGGCTCAGGCTGATGCTTGTGGCTGTGGCTGTGGCTTGATCTTCTTC	2046
Db	2113	GTGCTGACACTGCTGGGCTCAGGCTGATGCTTGTGGCTGTGGCTGTGGCTTGATCTTCTTC	2172
Qy	2047	TCTTTTGTCTTGTGACACTTTCAGCTGTGTGTCTTACTTTCATCTTTTCAAGATCAACTCC	2106
Db	2173	TCTTTTGTCTTGTGACACTTTCAGCTGTGTGTCTTACTTTCATCTTTTCAAGATCAACTCC	2232
Qy	2107	TTTCCAAAGGCTTCCTCATCTTCATCTGAGATCTGTGCAATGCGAGCTGACAGGCCCGAGTGTG	2166
Db	2233	TTTCCAAAGGCTTCCTCATCTTCATCTGAGATCTGTGCAATGCGAGCTGACAGGCCCGAGTGTG	2292
Qy	2167	CCCTCCCTCTGAAAGAGCACTCAGACTGCGCCAGGCTCCCATCAGCTGTGGGACGAC	2226
Db	2293	CCCTCCCTCTGAAAGAGCACTCAGACTGCGCCAGGCTCCCATCAGCTGTGGGAGAC	2352
Qy	2227	TGTGTCAAGCCGATTTAGAGCCTTCAAGGCCACCTGCGCATGTGATGAAAGAGATGTGGG	2286
Db	2353	TGTGTCAAGCCGATTTAGAGCCTTCAAGGCCACCTGCGCATGTGATGAAAGAGATGTGGG	2412
Qy	2287	CTCGTGTGACACTGTGCTGTGGCCCCCGAGCCAGGCCAAGCCCAAGCCCATGACGCGCAG	2346
Db	2413	CTCGTGTGACACTGTGCTGTGGCCCCCGAGCCAGGCCAAGCCCAAGCCCATGACGCGCAG	2472
Qy	2347	ACTTTGGAAGGCCCAACGACCATATGAGAGATATGGGCGCTTGTGCATATGTGTGACACCTCCG	2406
Db	2473	ACTTTGGAAGGCCCAACGACCATATGAGAGATATGGGCGCTTGTGCATATGTGTGACACCTCCG	2532
Qy	2407	GGGCTGGGGCTTTTGAATTTGGCCTTGGAGACCTACTCGGCTCTCACTCACTGCTCCACGAGA	2466
Db	2533	GG--CTGGGCTTTTGAATTTGGCCTTGGAGACCTACTCGGCTCTCACTCACTGCTCCACGAGA	2590
Qy	2467	CTCAGAAATGTGCGCGCCGATGTGCTGTAGAGTATCTGTCCCAATTTGTCCCAACCCAGCT	2526
Db	2591	CTCAGAAATGTGCGCGCCGATGTGCTGTAGAGTATCTGTCCCAATTTGTCCCAACCCAGCT	2650
Qy	2527	GGAAGGCTGTGTCTTCCTTACAACCCGTGGGCGCCAG--CCTCAATTGCTGGGGGACAGGCT	2585
Db	2651	GGAAGGCTGTGTCTTCCTTACAACCCGTGGGCGCCAGCCTCAATTGCTGGGGGACAGGCT	2710
Qy	2586	TGATATTTAGAGGTGTGACATCTCTTAAATCTGTGTGCCCCCTGTGGAGCAGAATGTGG	2645
Db	2711	TGATATTTAGAGGTGTGACATCTCTTAAATCTGTGTGCCCCCTGTGGAGCAGAATGTGG	2707
Qy	2646	CTTCAATGTCTGTGTCTTCGTGTGTGACACCTGTAGGGGCACTGTGAAATCCCTGTCAATTTTA	2705
Db	2771	CTTCAATGTCTGTGTCTTCGTGTGTGACACCTGTAGGGGCACTGTGAAATCCCTGTCAATTTTA	2833
Qy	2706	ACCTCAAGTGTGACCCAGAGGCGAATGTGGGCCCAAGGACAGACCTTCAAGGACAGAGCCCTG	2765
Db	2831	ACCTCAAGTGTGACCCAGAGGCGAATGTGGGCCCAAGGACAGACCTTCAAGGACAGAGCCCTG	2890
Qy	2766	GCGAGAGAGAGGCCCTTTTGTGCAGAGACACAGACAGAGCTCTGGCTACCTGTAGGCC	2821
Db	2891	GCGAGAGAGAGGCCCTTTTGTGCAGAGACACAGACAGAGCTCTGGCTACCTGTAGGCC	2946

RESULT 2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							</
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QY 1652 GGTACAACCTTACCGACCTGCTGTGAGAGTCTTTGGACCTAATGCTCCGCTACCTAC 1711  
 DB 1544 GGTACAACCTTACCGACCTGCTGTGAGAGTCTTTGGACCTAATGCTCCGCTACCTAC 1603  
 QY 1712 TCAAGCTGAGCGGCGATGAGGCTGGGGGCTCCCATCTTTCTGTGACGCTGTGAGGCTTGG 1771  
 DB 1604 TCAAGCTGAGCGGCGATGAGGCTGGGGGCTTTCTGTGACGCTGTGAGGCTTGG 1663  
 QY 1772 TGAATGTGACCACTATGAGGCGCCCATCTTGTGCTGTGACATGAGACTCCAGAGGCGCTCA 1831  
 DB 1664 TGAATGTGACCACTATGAGGCGCCCATCTTGTGCTGTGACATGAGACTCCAGAGGCGCTCA 1723  
 QY 1832 TCAACCTTCCATGCTGTGATCCGGGACCTCCGCTGTGACATGAGACTCCAGAGGCGCTCA 1891  
 DB 1724 CCAACCTTCCATGCTGTGATCCGGGACCTCCGCTGTGACATGAGACTCCAGAGGCGCTCA 1783  
 QY 1892 TCTTCAAGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1951  
 DB 1784 TCTTCAAGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1843  
 QY 1952 TGGGCTGCGGCGCCCAACCAAAAGTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2011  
 DB 1844 TGGGCTGCGGCGCCCAACCAAAAGTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1903  
 QY 2012 TGGGCTGCGGCGCCCAACCAAAAGTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2071  
 DB 1904 TGGGCTGCGGCGCCCAACCAAAAGTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1963  
 QY 2072 TTTGCTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2131  
 DB 1964 TTTGCTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2023  
 QY 2132 GGTACTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2191  
 DB 2024 GGTACTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2083  
 QY 2192 ACTGCGGCGGCGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2251  
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 QY 2252 GCGGCGGCGGCGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2311  
 DB 2144 CCAACCTTCCATGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2202  
 QY 2312 CGAGCGGCGGCGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2369  
 DB 2203 GTGCTGTGCGGCGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2262  
 QY 2370 GAGAGATGAGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2404  
 DB 2263 AAGGCTGAGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 2297

RESULT 3  
 BX381703 966 bp mRNA linear EST 26-APR-2004  
 LOCUS BX381703 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION Clone CS0D1068YN04 5-PRIME, mRNA sequence.

ACCESSION BX381703  
 VERSION BX381703.2 GI:46570764  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 966)  
 AUTHORS Li, W.-B., Gruber, C., Jessup, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 8, 2003 this sequence version replaced gi:30447018.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0D1068D020P1c=8113.f.  
 Location/Qualifiers  
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 /clone\_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 32.2%; Score 909.6; DB 5; Length 966;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-164;  
 Matches 932; Conservative 6; Mismatches 5; Indels 3; Gaps 2;

QY 1329 GGTCTCCCTGCTGAGGCTGAGGCGGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1388  
 DB 1 GGTCTCCCTGCTGAGGCTGAGGCGGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 60  
 QY 1389 GGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1448  
 DB 61 GGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 120  
 QY 1449 GGTGCGGCGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1508  
 DB 121 GGTGCGGCGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 180  
 QY 1509 GCTGCTGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1568  
 DB 181 GCTGCTGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 240  
 QY 1569 AGGCTGTGAGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1628  
 DB 241 AGGCTGTGAGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 300  
 QY 1629 CTTTCTGAGATGAGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1688  
 DB 301 CTTTCTGAGATGAGGCGGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 360  
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 QY 1749 TTTGCTGAGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1808  
 DB 421 TTTGCTGAGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 480  
 QY 1809 GCATGAGATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1868  
 DB 481 GCATGAGATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 540  
 QY 1869 CAGCTATATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1928  
 DB 541 CAGCTATATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 600  
 QY 1929 AGGCTATATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 1988  
 DB 601 AGGCTATATGAGGCGGCTGTGCTGTGCTGTGCTGTGACATGAGGCGCTGTGACATGAGACTCCAGAGGCGCTCA 660  
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[illegible]

RESULT 4	BX417949	971 bp	mRNA	linear	EST 01-MAY-2004
LOCUS	BX417949				
DEFINITION	BX417949 Homo sapiens PLACENTA		Homo sapiens cDNA	clone CS0DE014YB01	
ACCESSION	BX417949				
VERSION	BX417949.2				
KEYWORDS	5-PRIME, mRNA sequence.				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1. (bases 1 to 971)				
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On May 13, 2003 this sequence version replaced gi:30637675.				

Genoscope - Centre National de Séquençage  
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: [segrete@genoscope.cns.fr](mailto:segrete@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-015g (dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloneed  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies,  
division of Invitrogen.  
This sequence belongs to sequence cluster 8113.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS00DB014CA01QPlfc-8113.f>.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDBE014YB01"
/clone_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime and enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
library was not normalized."

```

	Query Match	Match Similarity	Score	DB	Length
Best Local Similarity	96.0%	Pred. No. 1,7e+163			
Matches	893	Conservative	28	Mismatches	9
				Indels	0
				Gaps	0

  

	Query	Match	Score	DB	Length
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42	GGAGACAGGCTTCGCTCTGTCAACAGGCTGAGACAGTGTGATCTTGGCTCAAC	101			
62	GTAACCTCCACCTCCCGGATTCAAGTAAATTTCATGCTCAGCTCCCAAGTAAGCTGGA	121			

Db	102	GTAACTCCACCTCCCGGGTTCAAGATATCTCATAGCTCTAGCTCCGAGTAGCTGGGA	161
QY	122	TTACAGGTGTGACCTTCACAAGATGACTCCGTGCGAGAAATATGACTCCCACTGCTGC	181
Db	162	TTACAGGTGTGACTTTCAGAGATGACTCCGTGCGAGAAATATGACTCCCACTGCTGC	221
QY	182	TGCAGACGACACTGTTCTGCTGATCTGCTTTCTGTTCCAAAGTGCCTCAGCGAGG	241
QY	242	GCCACAGGAAAGACTTTCGCTTCGACGCGACGAGGAAACAGACACAGAGAGAGCTTC	301
Db	282	GCCACAGGAAAGATTTTCGCTTCTTCCAGCGACGAGGAAACAGACACAGAGAGAGCTTC	341
QY	302	ACTTCAAAACCCACACAGACTTGCATCTTCATTCAGAACTCCGAGAGAGCTTCACAG	361
Db	342	ACTTCAAAACCCACACAGACTTGCATCTTCATTCAGAACTCCGAGAGAGCTTCACAG	401
QY	362	TCCATGCCCCCTTTTCCCTGACAGCCACCTGCTTCCCGATCCTTCCCGACCCGAGGGCC	421
Db	402	TCCATGCCCCCTTTTCCCTGACAGCCACCTGCTTCCCGATCCTTCCCGACCCGAGGGCC	461
QY	422	TCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGGAATTACATCTTCTATAGCA	481
Db	462	TCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGGAATTACATCTTCTATAGCA	521
QY	482	AGCGTGACTTCTGCTGATGATGACAAAGCTCTAGCCCTCTGCTTCCAGACACAGAGAG	541
Db	522	AGCGTGACTTCTGCTGATGATGACAAAGCTCTAGCCCTCTGCTTCCAGACACAGAGAG	581
QY	542	AGACCCCTGCTCAGAGGCCCCCGCTGTATGACACTTCCTGTCACCTCTGAGAGAGCTTC	601
Db	582	AGACCCCTGCTCAGAGGCCCCCGCTGTATGACACTTCCTGTCACCTCTGAGAGAGCTTC	641
QY	602	AGAACATCAGCCTGCCAGTGCACGCTTCACTTCTCCTTCCACAGTCTTCCACCA	661
Db	642	AGAACATCAGCCTGCCAGTGCACGCTTCACTTCTCCTTCCACAGTCTTCCACCA	701
QY	662	CGGCGCGCTCAAAATGCTCTCGTGTGACATGTGGGAGCTCAAAAGGAGCCTCAGGCTCTCA	721
Db	702	CGGCGCGCBCAAAATGCTCTCGTGTGASATGTGAGAGCTCAAAARAGACCTCAGAGCTCTCA	761
QY	722	GCCAGTTCCTGAACATCTCCAGAGAGGCTCAAGAGGCTCTCGAGCTGCCCGGCGAGCC	781
Db	762	GCCAGTTCCTGAACATCTCCAGAGAGGCTCAAGAGGCTCTCGAGCTGCCCGGCGAGCC	821
QY	782	AGCAGTTGCAGAGCCTGGAATCTGAATCTGACTCTGTGAAATTCATATGGGGGACATGTGCT	841
Db	822	AGCAGTTGCAGAGCCTKAGATGTGAAMTGACTCTGTGAAATTCATATGGGGGAGATGTGCT	881
QY	842	CCTTCGAGGAGAGCCGATTCAAACGCAAGATGAGAGCTCCAGGCCACAGCCGAGCTTC	901
Db	882	CCTTCGAGGAGAGCCGATTCAAACGCAAGATGAGAGCTCCAGGCCACAGCCGAGCTTC	941
QY	902	AGACCTTCACATCCACTCCCGGACAGAGG	931
Db	942	MRGACCTTCACATCCACTCCCGGAGAGG	971
RESULT 5			
EX384045		941 bp	linear
LOCUS	EX384045	941 bp	linear
DEFINITION	EX384045 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens		
ACCESSION	EX384045		
VERSION	EX384045.2		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 941)		



**AUTHORS** Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** On May 8, 2003 this sequence version replaced gi:30457193.

**CONTACT:** Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0DK003CD020P1&c=8113.f.

**FEATURES**  
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 /organism="Homo sapiens"  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 30.2%; Score 852.6; DB 5; Length 941;  
 Best Local Similarity 90.8%; Pred. No. 1.3e-153;  
 Matches 854; Conservative 51; Mismatches 35; Indels 1; Gaps 1;

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QY 122 TTACAGGTGTTGACTTCCAGAGTACTCCGTCGAGGAAATGACTCCCAAGTGGCTGC 181
Db 1 TTACAGGTGTTGACTTCCAGAGTACTCCGTCGAGGAAATGACTCCCAAGTGGCTGC 60
QY 182 TGCGAGGAGCACTGTTCTGCGAGTGTGCTCTTCTGATCCCAAGTGGCTGC 241
Db 61 TGCGAGGAGCACTGTTCTGCGAGTGTGCTCTTCTGATCCCAAGTGGCTGC 120
QY 242 GCCACAGGAGAACTTTGCTTCTGCGAGTGTGCTCTTCTGATCCCAAGTGGCTGC 301
Db 121 GCCACAGGAGAACTTTGCTTCTGCGAGTGTGCTCTTCTGATCCCAAGTGGCTGC 180
QY 302 ACTACAAACCCACACAGACTGCGGATCTCAATGAGAACTCCGAAAGGCGCTCACAG 361
Db 181 ACTACAAACCCACACAGACTGCGGATCTCAATGAGAACTCCGAAAGGCGCTCACAG 240
QY 362 TCCATGCCCTTCTGCGAGGCGCAAGCTGCTTCCGATCCTTCCCTGAGCCCAAGGCGC 421
Db 241 TCCATGCCCTTCTGCGAGGCGCAAGCTGCTTCCGATCCTTCCCTGAGCCCAAGGCGC 300
QY 422 TCTACCACTTCTGCTCTACTGAAACCGACATGCTGGAGATTATCTTCTCTATGGCA 481
Db 301 TCTACCACTTCTGCTCTACTGAAACCGACATGCTGGAGATTATCTTCTCTATGGCA 360
QY 482 AGCGTGACTTTCTGCTGATGACAAAGCTCTTACGCTCTCTGCTTCCAGACCGAGAG 541
Db 361 AGCGTGACTTTCTGCTGATGACAAAGCTCTTACGCTCTCTGCTTCCAGACCGAGAG 420
QY 542 AGAGCTGCTGAGGGCCCCCGCTGTAGCACTTCTGCACTCTGCTGAGAGGCTTC 601
Db 421 AGAGCTGCTGAGGGCCCCCGCTGTAGCACTTCTGCACTCTGCTGAGAGGCTTC 480
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QY 662 CGGCGCTGACATGCTGGGTGAGATGTCGAGGCTCAAAAGGAGCTTCAGCTCTCA 721

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Db 541 CGGCGCTGACAAARCTCGTGGACAMGTGGARCTCAAAAGAMCTCCAACTGCTCA 600
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Db 661 AACATTGACAAACCTGAGTCCAAATGATGCTCTGTGATCAATGAGGAGGAGAGGCTGT 720
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Db 721 CTTTCAGAGGAGACCGGATCAACGCAAGGATGAGAGCTCCAGCCCAAGCGGCTCC 780
QY 902 AGAAGCTGACATCCACTCCCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 961
Db 781 AAGAGCTGACAAACCTGAGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 962 TGCTGCTGCTGAGCACTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 841 TGCTGCTGCTGAGCACTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 1021 AGAATCTCTCTGTTGAGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1061
Db 901 AAGATCTCTCTGTTGAGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941

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**RESULT 6**  
 BX339034 981 bp mRNA linear EST 08-APR-2004  
 DEFINITION BX339034 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CS0D1066Y14 5-PRIME, mRNA sequence.

**ACCESSION** BX339034  
**VERSION** BX339034.2 GI:46281226  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

**REFERENCE**  
 1 (bases 1 to 981)  
 Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
**COMMENT** On May 2, 2003 this sequence version replaced gi:3043740.

**CONTACT:** Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0D1066Y14P01&c=8113.f.

## FEATURES

source  
 Location/Qualifiers  
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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 29.9%; Score 844.6; DB 5; Length 981;  
 Best Local Similarity 99.3%; Pred. No. 4.4e-152;  
 Matches 869; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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QY 4 CAGCAGGGTCTCGCTCTGTCAACAGAGCTGAGTGAAGTCTTGGCTCATCGT 63
DB 72 CTGAGAGGCTCTCGCTCTGTCAACAGAGCTGAGTGAAGTCTTGGCTCATCGT 131
QY 64 AACCTCAACCTCCCGGGTTCAGATGATTTCTATGCTTCAAGCTTCCGAGTATGCTGGGAT 123
DB 132 AACCTCAACCTCCCGGGTTCAGATGATTTCTATGCTTCAAGCTTCCGAGTATGCTGGGAT 191
QY 124 ACGAGTGTGACTTCAAGAGTGACTCGTGTGAGAGAAATGATCTCCGAGTGTGCTGTG 183
DB 192 ACGAGTGTGACTTCAAGAGTGACTCGTGTGAGAGAAATGATCTCCGAGTGTGCTGTG 251
QY 184 CAGACGACACTGTTCTCTGTGAGTCTGCTCTTCTGTGCTCAAGGTGCCAGAGGAGG 243
DB 252 CAGACGACACTGTTCTCTGTGAGTCTGCTCTTCTGTGCTCAAGGTGCCAGAGGAGG 311
QY 244 CACAGGGAAGACTTTCCTTTCTGACGACGAGGAAACCAAGACACAGAGAGAGCTCCAC 303
DB 312 CACAGGGAAGACTTTCCTTTCTGACGACGAGGAAACCAAGACACAGAGAGAGCTCCAC 371
QY 304 TACAACCCACACAGAGAGCTGAGATCTCATGAGAACTCCGAGAGGCTCTCAAGTC 363
DB 372 TACAACCCACACAGAGAGCTGAGATCTCATGAGAACTCCGAGAGGCTCTCAAGTC 431
QY 364 CATGCCCCCTTCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACG 423
DB 432 CATGCCCCCTTCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACG 491
QY 424 TACACACTTCTGCTCTACTGTGACGACGACGACGACGACGACGACGACGACGACG 483
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DB 552 CGTACTTCTTGTGAGTGAACAAAGCTCTAGCTCTCTCTCTCTCTCTCTCTCTCTCT 611
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DB 612 AGCTGTGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 671
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DB 672 AACATCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 731
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DB 792 CAGTTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 851
QY 784 CAGTTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843
DB 852 CAGTTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
QY 844 TTGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 878
DB 911 TTGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 944
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RESULT 7
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LOCUS AGENCOURT_7959188 NIH_MGC_112 Homo sapiens cDNA IMAGE:6110364
DEFINITION 5' mRNA sequence.
ACCESSION BU183659
VERSION BU183659.1 GI:22697643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  
1 (bases 1 to 932)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM2357 row: 1 column: 13  
High quality sequence stop: 665.  
Location/Qualifiers

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## ORIGIN

Query Match 29.9%; Score 843.2; DB 5; Length 932;  
Best Local Similarity 97.4%; Pred. No. 8.3e-152;  
Matches 899; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

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QY 1784 ACTATGCCCCCATATCTGGCTGTGATGAGTCCAGAGAGGAGGCTCATCACTTCA 1843
DB 12 ACTATGCCCCCATATCTGGCTGTGATGAGTCCAGAGAGGAGGCTCATCACTTCA 71
QY 1844 TGTGCTGATCCGAGAGCTCCCTGTGATCAATCAACCACTTGGCTCTTCAAGCTGG 1903
DB 72 TGTGCTGATCCGAGAGCTCCCTGTGATCAATCAACCACTTGGCTCTTCAAGCTGG 131
QY 1904 TGTGCTGATCCGAGAGCTCCCTGTGATCAATCAACCACTTGGCTCTTCAAGCTGG 1963
DB 132 TGTGCTGATCCGAGAGCTCCCTGTGATCAATCAACCACTTGGCTCTTCAAGCTGG 191
QY 1964 CCCACACCCAAAGTGTGATGATGCTGACATGCTGAGGAGGAGGAGGAGGAGGAGGAG 2023
DB 192 CCCACACCCAAAGTGTGATGATGCTGACATGCTGAGGAGGAGGAGGAGGAGGAGGAG 251
QY 2024 TGCCCTGGGCTTATCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2083
DB 252 TGCCCTGGGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 311
QY 2084 ACCCTTTCAGATCATCACTCTCTTCCAGAGGCTTCCATCTTCAATCTGATAGTGTCA 2143
DB 312 ACCCTTTCAGATCATCACTCTCTTCCAGAGGCTTCCATCTTCAATCTGATAGTGTCA 371
QY 2144 TGGGCTGACAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2203
DB 372 TGGGCTGACAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431
QY 2204 TCCCATAGCTCGGAGAGCACTGTGCAAGCGGATTTAGGCTTCCAGGCCAAGCTGGCC 2263
DB 432 TCCCATAGCTCGGAGAGCACTGTGCAAGCGGATTTAGGCTTCCAGGCCAAGCTGGCC 491
QY 2264 ATGTGATGAGAGAGATGCGGCTGTGCACTGCTGTGAGCCCGAGCCAGCCGAGCC 2323
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 QY 1619 TGGCTCACTGT 1678  
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 QY 1679 AGGTCTTGTGACCTGT 1737  
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 QY 1854 CCGGAGCTCCTGT 1873  
 Db 883 CCGGAGCTCCTGT 902  
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 ACCESSION CA488057  
 VERSION CA488057.1 GI:24948944  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 846)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@b-remail.nih.gov  
 Tissue Procurement: Kristi A. Eglund, Ira Pastan  
 CDNA Library Preparation: Kristi A. Eglund, Ira Pastan  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNL at:

http://image.llnl.gov  
 Plate: LLNL4278 row: e column: 09  
 High quality sequence stop: 694.  
 Location/Qualifiers  
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 /note="Vector: pCMV-Sport6, Site 1: EcoRV, Site 2: Not I;  
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 Directionally cloned. Priming method: oligo-dT. Average  
 insert size: 1800 bp. Library amplification: 26,000 fold.  
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
 Bungkok Lee & Ira Pastan. Discovery of new breast  
 cancer genes encoding membrane and secreted proteins.  
 Manuscript submitted."

ORIGIN  
 Query Match 28 5%; Score 805; DB 6; Length 846;  
 Best Local Similarity 97.7%; Pred. No. 1.9e-144;  
 Matches 844; Conservative 0; Mismatches 1; Indels 19; Gaps 2;

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 QY 1255 GGGTGTGAGACCGTCAAGAGAGAAACCCAACTTGTCTGTGTGCAACCACTTGTACTTGT 1314  
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 Db 121 TTTGCACTGT 180  
 QY 1375 CTCCTCTCAAGT 1434  
 Db 181 CTCCTCTCAAGT 240  
 QY 1435 TACCTGT 1494  
 Db 241 TACCTGT 282  
 QY 1495 GTGCAATGAACTGT 1554  
 Db 283 GTGCAATGAACTGT 342  
 QY 1555 CCGGTGACCTGT 1614  
 Db 343 CCGGTGACCTGT 402  
 QY 1615 TCCCTGTCAAGT 1674  
 Db 403 TCCCTGTCAAGT 462  
 QY 1675 GTGAGAGTCTTGTGACCTATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1734  
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 QY 1735 GGGTGTGAGACCGTCAAGAGAGAAACCCAACTTGTCTGTGTGCAACCACTTGTACTTGT 1793  
 Db 523 GGGTGTGAGACCGTCAAGAGAGAAACCCAACTTGTCTGTGTGCAACCACTTGTACTTGT 582  
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Db	703	CAACATGGCCATGTACACCAACATGGTGCTGCAGATCTCGGGCTTCGCCCCCAACACCA	762
Qy	1974	AAATGTGTCAATGTGCTGACATGCTGGGACCTCAGCTGAGTCTTGGGCTGCGCCCGAGC	2033
Db	763	AAATGTGTCAATGTGCTGACATGCTGGGACCTCAGCTGAGTCTTGGGCTGCGCCCGAGC	822
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Db	823	CTTGATCTTCTTCTCTCTTGGCTTC	846
 RESULT 13 BX337534                      820 bp        RNA           linear     EST 07-APR-2004 LOCUS                          BX337534 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA DEFINITION                    clone CSODI043YGI3 5-PRIME, mRNA sequence. ACCESSION                      BX337534 VERSION                        BX337534.2 GI:46273908 KEYWORDS                        EST. ORGANISM                        Homo sapiens (human) SOURCE                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; AUTHORS                        Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. TITLE                           L1.W.B., Gruber,C.; Jeesee,J. and Polayes,D. JOURNAL                        Full-length cDNA libraries and normalization COMMENT                        Unpublished (2001) On May 2, 2003 this sequence version replaced gi:30339619. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8113.f For more information about this cluster see <a href="http://www.genoscope.cns.fr/cdna?b=CSODI043AD07QPI&amp;c=8113.f">http://www.genoscope.cns.fr/cdna?b=CSODI043AD07QPI&amp;c=8113.f</a> .			
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ORIGIN Query Match                      28.5%; Score 803.4; DB 5; Length 820; Best Local Similarity    99.8%; Pred. No.3,8e-144; Matches    815; Conservative    0; Mismatches    6; Gaps    1;			
Qy	1472	AACCTGGGAGCTACACATCAAGTGAATGATGAACCTGCTGGCCGCTTCTCTGCTGG	1531
Db	5	AACCTGGGAGCTACACATCAAGTGAATGATGAACCTGCTGGCCGCTTCTCTGCTGG	64
Qy	1532	ACAAGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGAGCTTGAAGCTGGCTGCCAG	1591
Db	65	ACAAGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGAGCTTGAAGCTGGCTGCCAG	124
Qy	1592	CGAGTGCATCTTCCCTGCACTTCTCCCTGTACACCGAGCCCTTCCCTGAGATGGGCTCGAGG	1651
Db	125	CGAGTGCATCTTCCCTGCACTTCTCCCTGTACACCGAGCCCTTCCCTGAGATGGGCTCGAGG	184

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Db		185	GGTAAACCTTACCGACTGATGGTAGAGGTCTTTGGCACTTAATGCCCTGACTAC	244
OY		1712	TCAAAGTGAGCCCATAGGGCTGGGGCTTCCTCATTCTTGATGACGCTGATGGCCCTGG	1771
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OY		1772	TGATGTGACAACTAATAGCCCCCATCATCTTGACTGTGCATAGAAGTCCAGAAGGCTCA	1831
Db		305	TGATGTGACAACTAATAGCCCCCATCATCTTGACTGTGCATAGAAGTCCAGAAGGCTCA	364
OY		1832	TCTACCCCTTCATATGCTGTGATTCGGGATCTCCCTGGTGCAGTACATCAACAACTGGAGCC	1891
Db		365	TCTACCCCTTCATATGCTGTGATTCGGGATCTCCCTGGTGCAGTACATCAACAACTGGAGCC	424
OY		1892	TCTTCAAGCCGATGATTTCTGTTCAACATGGCCCAATGCTAGCACCATGATGGTCAAGATCC	1951
Db		425	TCTTCAAGCCGATGATTTCTGTTCAACATGGCCCAATGCTAGCACCATGATGGTCAAGATCC	484
OY		1952	TGCGGCTGCAGCCCCCAACCACAAAAGTGTCAATGTGCTGACATCACTGCTGGGCTCAGCC	2011
Db		485	TGCGGCTGCAGCCCCCAACCACAAAAGTGTCAATGTGCTGACATCACTGCTGGGCTCAGCC	544
OY		2012	TGGTCTTGGCCGCTGGCCCTGGAGCCCTGATCTTCTCTCTGCTTGGCTTGGCACTTCAGC	2071
Db		545	TGGTCTTGGCCGCTGGCCCTGGAGCCCTGATCTTCTCTCTGCTTGGCTTGGCACTTCAGC	604
OY		2072	TTGTGCTCTCTACCTTTTGACATCAATCACTCTTCCAAGGCTTCTCATCTTCAATCT	2131
Db		605	TTGTGCTCTCTACCTTTTGACATCAATCACTCTTCCAAGGCTTCTCATCTTCAATCT	664
OY		2132	GGTACTGATCCATAGCGCTGACAGCCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAG	2191
Db		665	GGTACTGATCCATAGCGCTGACAGCCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAG	723
OY		2192	ACTGAGCCAGGCTCCCCTCATAGCTCGGAGACACACTGTCTCAGCCGATCTTAGGCTTCCA	2251
Db		724	ACTGAGCCAGGCTCCCCTCATAGCTCGGAGACACACTGTCTCAGCCGATCTTAGGCTTCCA	783
OY		2252	GCCCACTGCCCACATGTGTATGAAGCAGAGATGGCGGCT	2288
Db		784	GCCCACTGCCCACATGTGTATGAAGCAGAGATGGCGGCT	820
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AUTHORS				
TITLE				
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COMMENT				
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NIH-MGC http://mhc.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: csgrabs-ro@mail.nih.gov				
Tissue Procurement: ATCC/DCTD/BTP				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
DNA Sequencing by: Agencourt Bioscience Corporation				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LNLN at:				
http://image.llnl.gov				
plate: LILAM13302 row: C column: 22				
High quality sequence stop: 608.				









93	17.2	78.2	1714	8	TE18SR	X98089 T. excavatum	166	16.8	76.4	137040	8	AP005806	AP005806 Oryza sat
94	17.2	78.2	1714	8	AP054904	AP054904 ChoicowmC	167	16.8	76.4	137218	2	OS0100037	AL606617 Oryza sat
95	17.2	78.2	2000	6	AX461405	AX461405 Sequence	168	16.8	76.4	137263	2	AC068740	AC068740 Homo sapi
96	17.2	78.2	3254	1	AY048197	AY048197 Frankia B	169	16.8	76.4	139868	8	AP004161	AP004161 Oryza sat
97	17.2	78.2	3619	9	BC010674	BC010674 Homo sapi	170	16.8	76.4	141674	2	AC080046	AC080046 Homo sapi
98	17.2	78.2	3641	6	C0716253	C0716253 Sequence	171	16.8	76.4	141782	8	AP005582	AP005582 Oryza sat
99	17.2	78.2	3643	9	H0MPTVPH	M68941 Human prote	172	16.8	76.4	143400	2	AC134927	AC134927 Homo sapi
100	17.2	78.2	4208	9	HSMB0876	BS648614 Homo sapi	173	16.8	76.4	143717	8	AC135920	AC135920 Oryza sat
101	17.2	78.2	31045	3	CEK088E3	AC104658 Homo sapi	174	16.8	76.4	143966	2	AC135920	AC135920 Oryza sat
102	17.2	78.2	39565	3	CEK088E3	Z81668 Caenorhabd	175	16.8	76.4	145254	8	AC114681	AC114681 Homo sapi
103	17.2	78.2	45319	1	PF1297913	AJ297913 Plasmid p	176	16.8	76.4	145818	8	AP005746	AP005746 Oryza sat
104	17.2	78.2	45675	8	AF039047	AF039047 Caenorhab	177	16.8	76.4	147836	8	AP003383	AP003383 Oryza sat
105	17.2	78.2	80472	8	AC007945	AC007945 Genomic B	178	16.8	76.4	151533	8	AC090873	AC090873 Homo sapi
106	17.2	78.2	87849	3	AC084453	AC084453 Caenorhab	179	16.8	76.4	151841	9	AC105233	AC105233 Homo sapi
107	17.2	78.2	99923	8	FS08	AC059990 Arabidops	180	16.8	76.4	152599	9	AC092745	AC092745 Homo sapi
108	17.2	78.2	110000	1	EX050951_42	Continuation (43 o	181	16.8	76.4	155702	8	OS0100137	OS0100137 Oryza sat
109	17.2	78.2	110000	2	AP006501_00	Continuation (43 o	182	16.8	76.4	155847	8	AC092766	AC092766 Homo sapi
110	17.2	78.2	139055	2	AC015719	AP006501 Cyanidior	183	16.8	76.4	158173	8	AC092778	AC092778 Oryza sat
111	17.2	78.2	158450	10	AC068911	AC015719 Homo sapi	184	16.8	76.4	163639	9	AC097493	AC097493 Homo sapi
112	17.2	78.2	163615	10	AC068913	AC068911 Mus muscu	185	16.8	76.4	163733	9	AC127526	AC127526 Homo sapi
113	17.2	78.2	164262	2	AC147723	AC068913 Mus muscu	186	16.8	76.4	164155	9	AC000385	AC000385 Homo sapi
114	17.2	78.2	172487	10	AL954375	AC147723 Pongo pyg	187	16.8	76.4	165187	5	AP003716	AP003716 Homo sapi
115	17.2	78.2	176578	2	AC041008	AC041008 Homo sapi	188	16.8	76.4	165987	5	AC147883	AC147883 Xenopus t
116	17.2	78.2	215416	10	AC129537	AC129537 Mus muscu	189	16.8	76.4	167576	2	AC147297	AC147297 Pan trogl
117	17.2	78.2	228267	2	AC096381	AC096381 Rattus no	190	16.8	76.4	171832	9	AC079942	AC079942 Homo sapi
118	17.2	78.2	233417	10	AL844416	AL844416 Mouse DNA	191	16.8	76.4	171862	8	AC130732	AC130732 Oryza sat
119	17.2	78.2	233417	2	AC111319	AC111319 Rattus no	192	16.8	76.4	172647	8	AC130732	AC130732 Oryza sat
120	17.2	78.2	243968	2	AC130131	AC111319 Rattus no	193	16.8	76.4	174171	9	AC068587	AC068587 Homo sapi
121	17.2	78.2	262936	2	AC121467	AC111319 Rattus no	194	16.8	76.4	174826	2	AC116562	AC116562 Homo sapi
122	17.2	78.2	280422	2	AC112901	AC112901 Rattus no	195	16.8	76.4	177303	2	AC135424	AC135424 Homo sapi
123	17.2	78.2	300029	8	AE016881	AE016881 Eremothec	196	16.8	76.4	177574	8	AC073648	AC073648 Homo sapi
124	17.2	78.2	300298	1	AE016788	AE016788 Pseudomon	197	16.8	76.4	180659	9	AC130349	AC130349 Homo sapi
125	17.2	78.2	302550	1	BE294137	BE294137 Pirellula	198	16.8	76.4	189043	2	AC130349	AC130349 Homo sapi
126	17.2	78.2	302988	1	AE017176	AE017176 Porphyrom	199	16.8	76.4	189043	2	AC034259	AC034259 Homo sapi
127	17.2	77.3	4529	3	AE017293	U72936 Caedra segyp	200	16.8	76.4	206192	2	AC121433	AC121433 Rattus no
128	17.2	77.3	27248	3	CEK088E3	Z68316 Caenorhabd	201	16.8	76.4	224391	2	AC126644	AC126644 Rattus no
129	16.8	76.4	334	9	HS0VH0316	Z68316 H. sapiens t	202	16.8	76.4	242195	2	AC097413	AC097413 Homo sapi
130	16.8	76.4	548	11	BA185446	BA185446 sqm14814	203	16.8	76.4	256899	2	AC097413	AC097413 Homo sapi
131	16.8	76.4	1361	8	AA0581481	AJ51481 Aberggill	204	16.8	76.4	292100	9	AF228730	AF228730 Homo sapi
132	16.8	76.4	16053	5	AK103360	AK103360 Oryza sat	205	16.8	76.4	295854	9	AF228730	AF228730 Homo sapi
133	16.8	76.4	2653	5	DRE245964	AJ25964 Danio rer	206	16.8	76.4	305584	2	AC095802	AC095802 Homo sapi
134	16.8	76.4	2702	9	AK091914	AK091914 Homo sapi	207	16.8	76.4	302085	1	AE017054	AE017054 Oryza sat
135	16.8	76.4	3193	9	CCU06928	U06928 Caulobacter	208	16.8	76.4	305518	2	AC006879	AC006879 Homo sapi
136	16.8	76.4	6515	9	AB007953	AB007953 Homo sapi	209	16.8	76.4	305518	2	AE016920	AE016920 Homo sapi
137	16.8	76.4	10275	8	YL16754	AJ006754 Yarrowia	210	16.8	76.4	305584	2	AC095802	AC095802 Homo sapi
138	16.8	76.4	10482	1	AE010498	AE010498 Pseudobacte	211	16.8	76.4	316339	2	AF102407	AF102407 Coutoubea
139	16.8	76.4	10792	1	AE011585	AE011585 Leptospir	212	16.4	74.5	410	8	AF105082	AF105082 Triclicum
140	16.8	76.4	11250	1	AE011947	AE011947 Xanthomon	213	16.4	74.5	427	8	AY096717	AY096717 Arabidops
141	16.8	76.4	11835	1	AE007258	AB007258 Sinorhizo	214	16.4	74.5	630	11	BV033294	BV033294 Arabidops
142	16.8	76.4	12680	1	AE005970	AE005970 Caulobact	215	16.4	74.5	630	11	BV033294	BV033294 Arabidops
143	16.8	76.4	14857	8	AC145385	AC145385 Oryza sat	216	16.4	74.5	656	8	AY083951	AY083951 Arabidops
144	16.8	76.4	30152	3	U28412	U28412 Caenorhabd	217	16.4	74.5	3768	14	BSU35768	BSU35768 Homo sapi
145	16.8	76.4	31110	3	CBRG14K24	AC084504 Caenorhabd	218	16.4	74.5	3768	14	BSU35768	BSU35768 Homo sapi
146	16.8	76.4	38102	8	AP0069750	AP0069750 Oryza sat	219	16.4	74.5	3783	14	BSU35768	BSU35768 Homo sapi
147	16.8	76.4	42380	8	AP005922	AP005922 Oryza sat	220	16.4	74.5	7295	14	PAU81259	PAU81259 Homo sapi
148	16.8	76.4	58408	1	AE017300_3	Continuation (4 of	221	16.4	74.5	10813	1	AE005928	AE005928 Homo sapi
149	16.8	76.4	61588	10	AL611970	AL611970 Mouse DNA	222	16.4	74.5	10813	1	AE005928	AE005928 Homo sapi
150	16.8	76.4	62726	2	AC084090	AC084090 Homo sapi	223	16.4	74.5	11415	1	AE004889	AE004889 Homo sapi
151	16.8	76.4	66521	2	AC137893	AC137893 Homo sapi	224	16.4	74.5	12746	1	AE001016	AE001016 Homo sapi
152	16.8	76.4	67261	2	AC103715	AC103715 Homo sapi	225	16.4	74.5	12746	1	AE001016	AE001016 Homo sapi
153	16.8	76.4	73103	2	AC0980106	AC0980106 Homo sapi	226	16.4	74.5	12746	1	AE001016	AE001016 Homo sapi
154	16.8	76.4	92171	9	AC004924	AC004924 Homo sapi	227	16.4	74.5	67943	3	AC006722	AC006722 Homo sapi
155	16.8	76.4	97556	9	AC079781	AC079781 Homo sapi	228	16.4	74.5	74328	8	F13K23	F13K23 Homo sapi
156	16.8	76.4	110000	8	AC092450_4	Continuation (5 of	229	16.4	74.5	80117	8	OS000006	OS000006 Homo sapi
157	16.8	76.4	110000	8	CR382129_14	Continuation (15 o	230	16.4	74.5	84487	2	AC125064	AC125064 Homo sapi
158	16.8	76.4	117046	8	CR382129_28	Continuation (29 o	231	16.4	74.5	85513	2	AP006696	AP006696 Homo sapi
159	16.8	76.4	117046	8	AC135600	AC135600 Oryza sat	232	16.4	74.5	97807	8	AB046436	AB046436 Arabidops
160	16.8	76.4	118553	8	AP005865	AP005865 Oryza sat	233	16.4	74.5	108720	1	AE017180_13	AE017180_13 Homo sapi
161	16.8	76.4	120139	9	AP003498	AP003498 Homo sapi	234	16.4	74.5	110000	8	LMF1CHR16_09	LMF1CHR16_09 Homo sapi
162	16.8	76.4	121340	9	AP003488	AP003488 Oryza sat	235	16.4	74.5	110000	8	CR380955_01	CR380955_01 Homo sapi
163	16.8	76.4	122130	2	AC005326	AC005326 Homo sapi	236	16.4	74.5	110000	8	CR382133_06	CR382133_06 Homo sapi
164	16.8	76.4	129043	2	AC128143	AC128143 Rattus no	237	16.4	74.5	110000	8	CR382133_06	CR382133_06 Homo sapi
165	16.8	76.4	132268	8	AC099733	AC099733 Oryza sat	238	16.4	74.5	111551	9	AL360178	AL360178 Human DNA

C 239	16.4	74.5	116952	8	OSJN00010	AL60453	Oryza sat	C 312	16.2	73.6	399	8	AF102466	AF102466	Orphium f
C 240	16.4	74.5	138940	8	AC063973	AC063973	Genomic S	C 313	16.2	73.6	399	8	AF102499	AF102499	Xestoea 1
C 241	16.4	74.5	144885	10	AT731766	AT731766	Mouse DNA	C 314	16.2	73.6	399	8	AF402222	AF402222	Centauriu
C 242	16.4	74.5	157947	8	OSJN00260	AT731614	Oryza sat	C 315	16.2	73.6	399	8	AF402231	AF402231	Centauriu
C 243	16.4	74.5	157947	8	OSJN00260	AT731614	Oryza sat	C 316	16.2	73.6	399	8	AY15678	AY15678	Centauriu
C 244	16.4	74.5	165339	3	CEY57A10A	AL117195	Caenorhab	C 317	16.2	73.6	399	8	AY15679	AY15679	Centauriu
C 245	16.4	74.5	180716	2	AC118169	AC118169	Rattus no	C 318	16.2	73.6	400	8	AF102402	AF102402	Centauriu
C 246	16.4	74.5	184810	10	AC090869	AC090869	Mus Muscu	C 319	16.2	73.6	400	8	AY156748	AY156748	Centauriu
C 247	16.4	74.5	225739	2	AC115646	AC115646	Rattus no	C 320	16.2	73.6	400	8	AY15681	AY15681	Centauriu
C 248	16.4	74.5	233364	2	BX571949	BX571949	Danio rer	C 321	16.2	73.6	400	8	AY15682	AY15682	Centauriu
C 249	16.4	74.5	236184	2	AC134125	AC134125	Rattus no	C 322	16.2	73.6	400	8	AY15683	AY15683	Centauriu
C 250	16.4	74.5	250918	2	AC106517	AC106517	Rattus no	C 323	16.2	73.6	400	8	AY15684	AY15684	Centauriu
C 251	16.4	74.5	252127	10	AC133576	AC133576	Mus muscu	C 324	16.2	73.6	401	8	CB4490197	CB4490197	Centauriu
C 252	16.4	74.5	260361	2	AC103347	AC103347	Rattus no	C 325	16.2	73.6	401	8	CL1490199	CL1490199	Centauriu
C 253	16.4	74.5	261844	2	AC103331	AC103331	Rattus no	C 326	16.2	73.6	401	8	AF402200	AF402200	Centauriu
C 254	16.4	74.5	264755	2	AC137353	AC137353	Rattus no	C 327	16.2	73.6	401	8	AF402211	AF402211	Centauriu
C 255	16.4	74.5	277000	1	SC0939109	AL939109	Streptomy	C 328	16.2	73.6	401	8	AF102476	AF102476	Centauriu
C 256	16.4	74.5	299925	1	AP005048	AP005048	Streptomy	C 329	16.2	73.6	402	8	AF402199	AF402199	Centauriu
C 257	16.4	74.5	300129	1	AE017309	AE017309	Desulfovib	C 330	16.2	73.6	402	8	AF402205	AF402205	Centauriu
C 258	16.4	74.5	349761	1	BX842646	BX842646	Bdellovib	C 331	16.2	73.6	402	8	AF402209	AF402209	Centauriu
C 259	16.2	73.6	155	8	AY201009	AY201009	Arabidops	C 332	16.2	73.6	402	8	AF402215	AF402215	Centauriu
C 260	16.2	73.6	168	8	CO434993	CO434993	Sequence	C 333	16.2	73.6	402	8	AF402216	AF402216	Centauriu
C 261	16.2	73.6	201	11	BY202831	BY202831	sqm21002	C 334	16.2	73.6	402	8	AF402217	AF402217	Centauriu
C 262	16.2	73.6	211	10	MUSPTKV	L25762	Mus muscu	C 335	16.2	73.6	402	8	AF402218	AF402218	Centauriu
C 263	16.2	73.6	242	5	AY266813	AY266813	Gadus mor	C 336	16.2	73.6	402	8	AF402219	AF402219	Centauriu
C 264	16.2	73.6	378	8	AY251749	AY251749	Centauriu	C 337	16.2	73.6	402	8	AF402220	AF402220	Centauriu
C 265	16.2	73.6	379	8	AY251750	AY251750	Centauriu	C 338	16.2	73.6	402	8	AF402248	AF402248	Centauriu
C 266	16.2	73.6	393	8	BE4490200	AL490200	Eustoma e	C 339	16.2	73.6	402	8	AF402250	AF402250	Centauriu
C 267	16.2	73.6	393	8	AY251741	AY251741	Ixanthus	C 340	16.2	73.6	402	8	AF402252	AF402252	Centauriu
C 268	16.2	73.6	394	8	AF102390	AF102390	Canescora	C 341	16.2	73.6	402	8	AY251733	AY251733	Centauriu
C 269	16.2	73.6	395	8	AF102416	AF102416	Eustoma r	C 342	16.2	73.6	402	8	AY251738	AY251738	Centauriu
C 270	16.2	73.6	396	8	AY251752	AY251752	Eustoma e	C 343	16.2	73.6	402	8	AY251739	AY251739	Centauriu
C 271	16.2	73.6	396	8	AY156685	AY156685	Schenkia	C 344	16.2	73.6	402	8	AY251746	AY251746	Centauriu
C 272	16.2	73.6	396	8	AY156686	AY156686	Schenkia	C 345	16.2	73.6	402	8	AY251747	AY251747	Centauriu
C 273	16.2	73.6	396	8	AY156687	AY156687	Zeltnera	C 346	16.2	73.6	402	8	CL4490198	CL4490198	Centauriu
C 274	16.2	73.6	396	8	AY156689	AY156689	Zeltnera	C 347	16.2	73.6	403	8	AF102477	AF102477	Centauriu
C 275	16.2	73.6	396	8	AY156690	AY156690	Zeltnera	C 348	16.2	73.6	403	8	AF102478	AF102478	Centauriu
C 276	16.2	73.6	396	8	AY156691	AY156691	Zeltnera	C 349	16.2	73.6	403	8	AF102479	AF102479	Centauriu
C 277	16.2	73.6	396	8	AY156692	AY156692	Zeltnera	C 350	16.2	73.6	404	8	AF402242	AF402242	Centauriu
C 278	16.2	73.6	396	8	AY156693	AY156693	Zeltnera	C 351	16.2	73.6	404	8	AY251734	AY251734	Centauriu
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C 280	16.2	73.6	396	8	AY156695	AY156695	Zeltnera	C 353	16.2	73.6	405	8	AF102393	AF102393	Centauriu
C 281	16.2	73.6	396	8	AY156696	AY156696	Zeltnera	C 354	16.2	73.6	405	8	AF402244	AF402244	Centauriu
C 282	16.2	73.6	397	8	AF402228	AF402228	Centauriu	C 355	16.2	73.6	405	8	AF402249	AF402249	Centauriu
C 283	16.2	73.6	397	8	AY156680	AY156680	Gyrandra	C 356	16.2	73.6	406	8	AF402251	AF402251	Centauriu
C 284	16.2	73.6	397	8	AY156688	AY156688	Zeltnera	C 357	16.2	73.6	406	8	MP4490241	MP4490241	Centauriu
C 285	16.2	73.6	398	8	OPR490244	AF490244	Orphium f	C 358	16.2	73.6	407	8	AF402240	AF402240	Centauriu
C 286	16.2	73.6	398	8	AF102394	AF102394	Centauriu	C 359	16.2	73.6	407	8	AY251729	AY251729	Centauriu
C 287	16.2	73.6	398	8	AF402203	AF402203	Centauriu	C 360	16.2	73.6	407	8	AY251731	AY251731	Centauriu
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## ALIGNMENTS

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 VERSION JP 2001512011-A/109.  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Edwards J.B.D.M., Duclet A., and Lacroix B.  
 TITLES 5' EST of tissue-nonspecific secretory protein  
 JOURNAL Patent: JP 2001512011-A 109 21-AUG-2001;  
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 OS Homo sapiens (human)  
 PN JP 2001512011-A/109  
 PD 21-AUG-2001  
 PR 31-JUL-1998 JP 2000505289  
 PF 01-AUG-1997 US 08/905135  
 PI JEAN BAPTISTE DUMAS; MILNE EDWARDS; AYMERIC DUCLEART; BRUNO PI  
 LACROIX  
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Db 369 TTCGAGTTCGATGAGAT 349

RESULT 2  
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LOCUS Sequence 17088 from Patent WO0157278.  
DEFINITION CQ081288  
ACCESSION CQ081288.1 GI:41051157  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human hela cells or other human  
cervical epithelial cells  
JOURNAL Patent: WO 0157278-A 17088 09-AUG-2001;  
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LOCUS Sequence 24693 from Patent WO0157272.  
DEFINITION CQ115834  
ACCESSION CQ115834  
VERSION CQ115834.1 GI:41085704  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 24693 09-AUG-2001;  
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 122 TTCGAGTTCGATGAGAT 102

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LOCUS Sequence 24624 from Patent WO0157276.  
DEFINITION CQ154602  
ACCESSION CQ154602  
VERSION CQ154602.1 GI:41161954  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 24624 09-AUG-2001;  
Aeomica, Inc. (US)  
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ACCESSION CQ187133
VERSION CQ187133.1 GI:41182145
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human heart
Aeomica, Inc. (US)
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Db 122 TTCGAGTTCGATGAGAT 102

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ACCESSION CQ237857
VERSION CQ237857.1 GI:41221137
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
JOURNAL ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
Aeomica, Inc. (US)
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DEFINITION Sequence 23740 from Patent WO0157277.
ACCESSION CQ275479
VERSION CQ275479.1 GI:41248083
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human fetal liver
Aeomica, Inc. (US)
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ACCESSION CQ312440
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KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
JOURNAL analysis of gene expression in human lung
Aeomica, Inc. (US)
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EVALU0 0.00e+00"

Query Match 95.5%; Score 21; DB 6; Length 423;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
Db 122 TTGGAGTTCTCGATGAGAT 102

RESULT 9  
CQ349899/c 423 bp DNA linear PAT 23-JAN-2004  
LOCUS CQ349899  
DEFINITION Sequence 23993 from Patent WO0157275.  
ACCESSION CQ349899  
VERSION CQ349899.1 GI:41238970  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 23993 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source location/Qualifiers  
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/note="WAP TO AC018552.2-EXPRESSED IN BRAIN, SIGNAL =  
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EVALU0 0.00e+00"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 423;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
Db 122 TTGGAGTTCTCGATGAGAT 102

RESULT 10  
CQ407379/c 493 bp DNA linear PAT 23-JAN-2004  
LOCUS CQ407379  
DEFINITION Sequence 14450 from Patent WO0170979.  
ACCESSION CQ407379  
VERSION CQ407379.1 GI:41315160  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Lee, J. and Lillie, J.  
TITLE Genes, compositions, kits, and method for identification,  
assessment, prevention, and therapy of ovarian cancer  
JOURNAL Patent: WO 0170979-A 14450 27-SEP-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..493  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 493;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
Db 416 TTGGAGTTCTCGATGAGAT 396

RESULT 11  
CQ072149/c 582 bp DNA linear PAT 20-JAN-2004  
LOCUS CQ072149  
DEFINITION Sequence 7949 from Patent WO0157278.  
ACCESSION CQ072149  
VERSION CQ072149.1 GI:41042018  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human hela cells or other human  
cervical epithelial cells  
JOURNAL Patent: WO 0157278-A 7949 09-AUG-2001;  
Aeomica, Inc. (US)  
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Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 12  
CQ102837/c 582 bp DNA linear PAT 21-JAN-2004  
LOCUS CQ102837  
DEFINITION Sequence 11696 from Patent WO0157272.  
ACCESSION CQ102837  
VERSION CQ102837.1 GI:41071863  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 11696 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source location/Qualifiers  
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/mol\_type="unassigned DNA"  
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7.2"

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Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
 |||||  
 Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 13  
 CQ141717/c 582 bp DNA linear PAT 21-JAN-2004  
 LOCUS Sequence 11739 from Patent WO0157276.  
 DEFINITION CQ141717  
 ACCESSION CQ141717.1 GI:41099089  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 JOURNAL analysis of gene expression in human bone marrow  
 Patent: WO 0157276-A 11739 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AC018552.2-EXPRESSED IN BONE MARROW, SIGNAL  
 = 5.4"

ORIGIN  
 Query Match 95.5%; Score 21; DB 6; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
 |||||  
 Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 14  
 CQ177316/c 582 bp DNA linear PAT 21-JAN-2004  
 LOCUS Sequence 8712 from Patent WO0157274.  
 DEFINITION CQ177316  
 ACCESSION CQ177316  
 VERSION CQ177316.1 GI:41172055  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 JOURNAL analysis of gene expression in human heart  
 Patent: WO 0157274-A 8712 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..582  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AC018552.2-EXPRESSED IN HEART, SIGNAL = 4.7"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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 Db 227 TTGGAGTTCTCGATGAGAT 207

Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 15  
 CQ225007/c 582 bp DNA linear PAT 21-JAN-2004  
 LOCUS Sequence 11846 from Patent WO0157273.  
 DEFINITION CQ225007  
 ACCESSION CQ225007  
 VERSION CQ225007.1 GI:41207461  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
 (03.10.00)<150> US 60/236,359<151> 27 September 2000  
 (27.09.00)<150> US 60/234,687<151> 21 September 2000  
 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
 Molecular Dynamics Sequence Listing Engine  
 Patent: WO 0157273-A 11846 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..582  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AC018552.2-EXPRESSED IN ADULT LIVER, SIGNAL  
 = 5.7"

ORIGIN  
 Query Match 95.5%; Score 21; DB 6; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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 Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 16  
 CQ263027 582 bp DNA linear PAT 23-JAN-2004  
 LOCUS Sequence 11288 from Patent WO0157277.  
 DEFINITION CQ263027  
 ACCESSION CQ263027  
 VERSION CQ263027.1 GI:41235507  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
 TITLE Human genome-derived single exon nucleic acid probes useful for  
 JOURNAL analysis of gene expression in human fetal liver  
 Patent: WO 0157277-A 11288 09-AUG-2001;  
 Aeomica, Inc. (US)  
 FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="MAP TO AC018552.2-EXPRESSED IN FETAL LIVER, SIGNAL  
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ORIGIN  
 Query Match 95.5%; Score 21; DB 6; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 17  
LOCUS CQ300060/c 582 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 11165 from Patent WO0186003.  
ACCESSION CQ300060  
VERSION CQ300060.1 GI:41260637  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human lung  
Patent: WO 0186003-A 1165 15-NOV-2001;  
Aecomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN LUNG, SIGNAL = 6.5"

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 18  
LOCUS CQ337293/c 582 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 11387 from Patent WO0157275.  
ACCESSION CQ337293  
VERSION CQ337293.1 GI:41286364  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human brain  
Patent: WO 0157275-A 11387 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN BRAIN, SIGNAL = 7.8"

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 227 TTGGAGTTCTCGATGAGAT 207

RESULT 19  
LOCUS CQ780635/c 739 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 775 from Patent EP1396543.  
ACCESSION CQ780635  
VERSION CQ780635.1 GI:45536707  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
Koga, H.  
TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Research Association for Biotechnology (JP)  
Patent: EP 1396543-A 775 10-MAR-2004;  
Location/Qualifiers  
1..739  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 739;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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Db 430 TTGGAGTTCTCGATGAGAT 410

RESULT 20  
LOCUS CQ782177/c 739 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 2317 from Patent EP1396543.  
ACCESSION CQ782177  
VERSION CQ782177.1 GI:45538233  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
Koga, H.  
TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Research Association for Biotechnology (JP)  
Patent: EP 1396543-A 2317 10-MAR-2004;  
Location/Qualifiers  
1..739  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 739;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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Db 430 TTGGAGTTCTCGATGAGAT 410

RESULT 21  
LOCUS BD125344/c 739 bp DNA linear PAT 18-SEP-2002

DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD125344  
 VERSION BD125344.1 GI:23220289  
 KEYWORDS JP 2002017375-A/775.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 739)  
 Ota.T., Nishikawa.T., Isogai.T., Hayashi.K., Ishii.S., Kawai.Y., Wakamatsu.A., Sugiyama.T., Nagai.K., Kojima.S., Otsuki.T. and Koga.H.  
 Primer for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002017375-A 775 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002017375-A/775  
 PD 22-JAN-2002  
 PP 07-JUL-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI, HISASHI KOGA  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
 Primer for synthesizing full-length cDNA and use thereof FH Key  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'

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 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
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 DB 430 TTCGAGTTCTCGATGAGAT 410

RESULT 22  
 BD126886/c 739 bp DNA linear PAT 18-SEP-2002  
 LOCUS BD126886  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD126886  
 VERSION BD126886.1 GI:23221831  
 KEYWORDS JP 2002017375-A/2317.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 739)  
 Ota.T., Nishikawa.T., Isogai.T., Hayashi.K., Ishii.S., Kawai.Y., Wakamatsu.A., Sugiyama.T., Nagai.K., Kojima.S., Otsuki.T. and Koga.H.  
 Primer for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002017375-A 2317 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002017375-A/2317  
 PD 22-JAN-2002  
 PP 07-JUL-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI

SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI, HISASHI KOGA  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
 Primer for synthesizing full-length cDNA and use thereof FH Key  
 Location/Qualifiers  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'

FEATURES  
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 /organism='Homo sapiens (human)'  
 /mol\_type='genomic DNA'  
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ORIGIN  
 Query Match 95.5%; Score 21; DB 6; Length 739;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
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 DB 430 TTCGAGTTCTCGATGAGAT 410

RESULT 23  
 AX136607/c 745 bp DNA linear PAT 30-MAY-2001  
 LOCUS AX136607  
 DEFINITION Sequence 529 from Patent EP1067182.  
 ACCESSION AX136607  
 VERSION AX136607.1 GI:14273011  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 745)  
 Ota.T., Isogai.T., Nishikawa.T., Kawai.Y., Sugiyama.T. and Hayashi.K.  
 Secretory protein or membrane protein  
 Patent: EP 1067182-A 529 10-JAN-2001;  
 Helix Research Institute (JP)  
 Location/Qualifiers  
 FT source 1..745  
 /organism='Homo sapiens (human)'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:9606'

ORIGIN  
 Query Match 95.5%; Score 21; DB 6; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
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 DB 453 TTCGAGTTCTCGATGAGAT 433

RESULT 24  
 BD123847/c 745 bp DNA linear PAT 18-SEP-2002  
 LOCUS BD123847  
 DEFINITION Secretory protein or membrane protein.  
 ACCESSION BD123847  
 VERSION BD123847.1 GI:23218792  
 KEYWORDS JP 2002017376-A/356.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 745)  
 Ota.T., Isogai.T., Nishikawa.T., Kawai.Y., Sugiyama.T. and Hayashi.K.

TITLE  
JOURNAL  
SECRETORY protein or membrane protein  
Patent: JP 2002017376-A 356 22-JAN-2002;  
HEILIX RESEARCH INSTITUTE  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002017376-A/356  
PD 22-JAN-2002  
PF 07-JUL-2000 JP 2000253173  
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU  
PI SUGIYAMA,  
PI KOJI HAYASHI  
PC  
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/00,  
10, C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N5/00 CC  
PC C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N5/00 CC  
SECRETORY protein or membrane protein  
FH Key Location/Qualifiers  
FT source 1..745  
FT /organism='Homo sapiens (human)'.  
1..745  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 745;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
453 TTCGAGGTTCTCGATGAGAT 433  
|||||

RESULT 25  
LOCUS CQ755181 2061 bp DNA linear PAT 01-MAR-2004  
DEFINITION Sequence 74 from Patent EP1375515.  
ACCESSION CQ755181  
VERSION CQ755181.1 GI:44846115  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Fukushima, D., Shibayama, S. and Tada, H.  
TITLE Polypeptide, cDNA encoding the same, and use thereof  
JOURNAL Patent: EP 1375515-A 74 02-JAN-2004;  
ONO PHARMACEUTICAL CO., LTD. (JP)  
FEATURES  
source 1..2061  
/organism='Homo sapiens'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:9606'

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 2061;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
186 TTCGAGGTTCTCGATGAGAT 166  
|||||

RESULT 26  
LOCUS AX029423 2082 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 3 from Patent WO9915551.  
ACCESSION AX029423  
VERSION AX029423.1 GI:10190216  
KEYWORDS

SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Herzog, H.  
TITLE Novel receptor  
JOURNAL Patent: WO 9915551-A 3 01-APR-1999;  
GARVAN INST MED RES (AU); HERZOG HERBERT (AU)  
FEATURES  
source 1..2082  
/organism='Homo sapiens'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:9606'

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 2082;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
186 TTCGAGGTTCTCGATGAGAT 166  
|||||

RESULT 27  
LOCUS AX429262 2082 bp DNA linear PAT 02-JUL-2002  
DEFINITION Sequence 1 from Patent WO0234781.  
ACCESSION AX429262  
VERSION AX429262.1 GI:21540569  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Berger, C., Van Rander, J. and Tulp, M.T.M.  
TITLE Human G-protein coupled diadenosine tetraphosphate receptor (AP4AR)  
JOURNAL Patent: WO 0234781-A 1 02-MAY-2002;  
SOLVAY PHARM GMBH (DE)  
FEATURES  
source 1..2082  
/organism='Homo sapiens'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:9606'

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 2082;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
186 TTCGAGGTTCTCGATGAGAT 166  
|||||

RESULT 28  
LOCUS BD062445 2082 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel receptor.  
ACCESSION BD062445  
VERSION BD062445.1 GI:22608048  
KEYWORDS JP 2001513653-A/1.  
SOURCE Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Herzog, H.  
TITLE Novel receptor  
JOURNAL Patent: JP 2001513653-A 1 04-SEP-2001;  
GARVAN INSTITUTE OF MEDICAL RESEARCH

COMMENT OS Homo sapiens (human)  
 PN JP 2001513653-A/1  
 PD 04-SEP-2001  
 PF 24-SEP-1998 JP 1999518348  
 PR 24-SEP-1997 AU PO 9386  
 PI HERBERT HERZOG  
 PC C07K7/06, C07K14/705, C07K16/28, C12N15/12, C12N5/10, C12P21/02, PC  
 A01K67/027  
 PC GOIN33/68, C07H21/04  
 CC  
 FH Key Location/Qualifiers  
 FEATURES  
 source 1..2082  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1..2082  
 CDS

Query Match 95.5%; Score 21; DB 6; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
 |||||  
 DB 186 TTCCGAGTTCTCGATGAGAT 166

RESULT 29  
 BT007311/c 2082 bp mRNA linear PRI 13-MAY-2003  
 LOCUS Homo sapiens G protein-coupled receptor 56 mRNA, complete cds.  
 DEFINITION BT007311  
 ACCESSION BT007311.1 GI:30583460  
 VERSION FLI CDNA.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.  
 TITLE Cloning of human full-length CDS in BD Creator(TM) System Donor vector  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA  
 COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BP in-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.  
 Clone distribution: http://bioinfo.clontech.com/orfclones.  
 Location/Qualifiers  
 1..2082  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1..2082

/codon\_start=1  
 /product="G protein-coupled receptor 56"  
 /protein\_id="AAP35975.1"  
 /db\_xref="GI:30583461"  
 /translation="MTPQSLITQTLFLSLFLVQAGRGHREDPRFCGQRNQTIRSS  
 SLHYKPTPLSRISSENSREALVYHAPPAHAPASRPDPDRLGYHCLVYNNRAGRLH  
 LLYGKRDPLSRKASSLCFQHOESLQAGPLLATVSTWSMNPONISLPSASPTES  
 PHSPPTTAHNNASVDMCEKRLDQLISGLKHPKRSRRPSAASQGLQSLSKLTS  
 VFMGMVAFSEEDRINATVYKQLPDGTGDDLIHNSQBERQSIIMEYSVLTPTLFR  
 TGRSGEAEKRLLLVDFSSQALFQDNSSHVIGEKVLGIVQNTKANTLTERVVLTPQ  
 HOLQKGVTLQCFWVEDPTLSFGHMSAGCEVTRRTQSCFNHLYTFAVLMVS  
 VEYDAVHKHYLSLSYGCVSALCLVTLAALCSRVPDPCRRKRDYTIKVHMLL  
 LAVFLDPTSLISEPVALGSEACGSAIPLHFSILTCISMGLGVNLYRAVVEVF  
 GYVVPQYILKLGAMGWPPIPLVTVALVDVNYGPIILAVHRTPGGVYPSMCWID  
 SLVSYITNGLBSLVFLPMNMAATVNVQILRIKRPRTKRSVLTLLGSLVGLPWA  
 LIFFSASGTFPLVLYLFSITTSFGFLFTYWMRLQARGPSPDKNSDARLP  
 ISGSGTSSSRI"

Query Match 95.5%; Score 21; DB 9; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
 |||||  
 DB 186 TTCCGAGTTCTCGATGAGAT 166

RESULT 30  
 BT009896/c 2082 bp mRNA linear SYN 02-AUG-2003  
 LOCUS Synthetic construct Homo sapiens G protein-coupled receptor 56  
 DEFINITION BT009896  
 ACCESSION BT009896.1 GI:32880134  
 VERSION FLI CDNA.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUL-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, California 94303, USA  
 COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BP in-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.  
 Clone distribution: http://bioinfo.clontech.com/orfclones.  
 Location/Qualifiers  
 1..2082  
 /organism="Synthetic construct"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:32630"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1..2082



CDS

1..>2082  
/note="Mutations: 2081:stop->L"  
/codon\_table=1  
/product="g protein-coupled receptor 56"  
/protein\_id="AAP8898.1"  
/db\_xref="GI:32860135"  
/translation="MTPOSILQTTLEFLISLFLVGAHGRGHREDFRFCQOROTHR  
SLHYKTPDRLRISTENSEALTVHAPPAAPARSPDPGIVHPCLYMRHGRHL  
LVYKRPDLSDKASSLICFQHQBESLAQGPLATSTTSMWSRONISLPSAASPTPS  
FHPSPHTAANAASVDMCELRDLQLSLQFLHPOKASRPSAASQQLSLESFLTS  
VRFWGDAWEKELRINATVMTLQPLAQDLHHSROEQLMEYSVLLPRLFOR  
TKSGSGAEKELLVDFSSQALFQDKNSHYLGIVONTKANTLPEVVLTEQ  
HQLQPKVTLQCFWVEDPTLSPHMSAGCEYRRETQSCFNHLTYPAVIVSS  
VEDAVHRYVLSLISVGCVCVSAACIVTIAACRYPLPCRRKRPDYTLKMNLL  
LAVPLDTSFLISEPVALTGSSEGRASAIILHBSLILCLSMGLEGNLYRIVVEF  
GTVPVGLIKLSANGWGPFLVTLVVALVDNDGFIILAVHRTPEGYTYSMCYIR  
SLVSYITNLGLFSLVFLFNMMALMTVMVQILRLRPHTKWSHVLTLGLSLVGLPMA  
LIPFSFAGTFQLVLYLFSIITSFQGLIFITWMSMLQARGSPSLKNSDSARLP  
ISSGSTSSRL"

ORIGIN

Query Match 95.5%; Score 21; DB 12; Length 2082;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 186 TTCGAGTTCGATGAGAT 166

RESULT 31  
LOCUS CQ715549 2821 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 1483 from Patent WO02068579.  
ACCESSION CQ715549  
VERSION CQ715549.1 GI:42276406  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
human genes or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 1483 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES  
source Location/Qualifiers  
1..2821  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2821;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 348 TTCGAGTTCGATGAGAT 328

RESULT 32  
LOCUS AX298003 2822 bp DNA linear PAT 26-NOV-2001  
DEFINITION Sequence 1 from Patent WO0183558.  
ACCESSION AX298003  
VERSION AX298003.1 GI:17128089  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Brennan, J.C. and Hart, K.A.  
TITLE Agonists/antagonists of the gp56 receptor as appetite control  
agents  
JOURNAL Patent: WO 0183558-A 1 08-NOV-2001;  
Astrazeneca AB (SE)  
FEATURES  
source Location/Qualifiers  
1..2822  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 348 TTCGAGTTCGATGAGAT 328

RESULT 33  
LOCUS AX549232 2822 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 517 from Patent WO02061087.  
ACCESSION AX549232  
VERSION AX549232.1 GI:25813927  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides  
JOURNAL Patent: WO 02061087-A 517 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..2822  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 348 TTCGAGTTCGATGAGAT 328

RESULT 34  
LOCUS AF106858 2822 bp mRNA linear PRI 17-MAY-1999  
DEFINITION Homo sapiens G-protein-coupled receptor (GPR56) mRNA, complete cds.  
ACCESSION AF106858  
VERSION AF106858.1 GI:4836764  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Liu, M., Parker, R.M., Darby, K., Eyre, H.J., Copeland, N.G.,  
Crawford, J., Gilbert, D.J., Sutherland, G.R., Jenkins, N.A. and

TITLE Herzog, H.  
JOURNAL GPR56, a novel secretin-like human G-protein-coupled receptor gene  
MEDLINE Genomics 55 (3), 296-305 (1999)  
99168899

REFERENCE 10049584  
2 (bases 1 to 2822)

AUTHORS Herzog, H.  
TITLE Direct Submision  
JOURNAL Submitted (17-MAR-1999) Neurobiology, Garvan Institute, 384  
Victoria St., Sydney, NSW 2010, Australia

FEATURES  
SOURCE Location/Qualifiers

1..2822  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/map="q31"  
1..2822  
/gene="GPR56"  
163..2244  
/gene="GPR56"  
/note="SLR32"  
/codon\_start=1  
/product="G-protein-coupled receptor"  
/protein\_id="AB030545.1"  
/db\_xref="GI:4836765"  
/translation="MTPQSLQTTLELLFLVQAGHGRHEDRFCSQRNQHRS  
SLHYKTPDLRISENSBEALTVHAPPAHPSRFPDPRGLYHPCLYMNRHAGRLH  
LHYKRPDLSDASGLCFQOBSLAQPPPLATSVSWSPQNISLPSAASFPS  
FHSPPHTAHNASVDMCELRKDLQISLQFHKOKARRPSAPAOQOSLEKLT  
VAPMGMSFEEEDRINATYWKLOPTGLDTHSROEBOSEIMESVTLPEPTFOR  
TKRSGEAKRLVDPSSCALFQDNSSCVLEKVLGYVQNTKANTPEVLTFO  
HQLQPNVTLQCFWVEDPTLSFGHSSAGCEVRETQSCFNHLYFAVAMVS  
VEVDVAKHYLSLSYGCVSALACLVTIAVLCRVPVPCRRKRDYTIKVMNL  
LAVFLDTSFLISEPVALTGSEACRASAIFLHFSLTLCISWMLGYNLYLVAVE  
GTYVPGYTLKLSMGWGPPIPLTVLAVDVNDYGPILIAVHRTPEGVLYPSMCVRD  
SLVSYTINIGLSIVLPMAMATMVQVQILRLRPHRTOKRSHVLTLLGSLVTLGPM  
LIFPSFASGTFQLVLYLPSITTSFQGLFIFTYWMRLQARSGPPLKSNDCALP  
ISSGSTSSSRI"

## ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 348 TTTCGAGTTCTCGATGAGAT 328

RESULT 35  
AX029424/c 2834 bp DNA linear PAT 16-SEP-2000  
LOCUS AX029424  
DEFINITION Sequence 4 from Patent WO9915551.  
ACCESSION AX029424  
VERSION AX029424.1 GI:10190217  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Herzog, H.  
AUTHORS Novel receptor  
TITLE Patent: WO 9915551-A 4 01-APR-1999;  
JOURNAL GARVAN INST MED RES (AU) ; HERZOG HERBERT (AU)  
FEATURES Location/Qualifiers  
1..2834  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2834;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 354 TTTCGAGTTCTCGATGAGAT 334

RESULT 36  
BD062446/c 2834 bp DNA linear PAT 27-AUG-2002  
LOCUS BD062446  
DEFINITION Novel receptor.  
ACCESSION BD062446  
VERSION BD062446.1 GI:22608049  
KEYWORDS JP 2001513653-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2834)  
AUTHORS Herzog, H.  
TITLE Novel receptor  
JOURNAL Patent: JP 2001513653-A 2 04-SEP-2001;  
COMMENT GARVAN INSTITUTE OF MEDICAL RESEARCH  
OS Homo sapiens (human)  
PN JP 2001513653-A/2  
PD 04-SEP-2001  
PF 24-SEP-1998 JP 1999518348  
PR 24-SEP-1997 AU PO 9386  
PI HERBERT HERZOG  
PC C07K7/06, C07K14/705, C07K16/28, C12N15/12, C12N5/10, C12P21/02, PC  
A01K67/027, PC  
G01N33/68, C07H21/04

FEATURES  
source Location/Qualifiers.  
FH Key

1..2834  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 95.5%; Score 21; DB 6; Length 2834;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 354 TTTCGAGTTCTCGATGAGAT 334

RESULT 37  
AX965647/c 3564 bp DNA linear PAT 15-JAN-2004  
LOCUS AX965647  
DEFINITION Sequence 75 from Patent EP1375515.  
ACCESSION AX965647  
VERSION AX965647.1 GI:40974984  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Fukushima, D.M., Shibayama, S.M., and Tada, H.M.  
AUTHORS Polypeptide, cDNA encoding the same, and use thereof  
TITLE Patent: EP 1375515-A 75 02-JAN-2004;  
JOURNAL ONO PHARMACEUTICAL CO., LTD. (JP)  
FEATURES Location/Qualifiers  
1..3564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

## CDS

43..2106  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAFO6561.1"  
/db\_xref="gi:40974985"  
/translation="MTPTSLQTLTFLTSLFLNCGARGHREDPPSCGNQTHRS  
SLHYPTDLRISTENSEBALTVAPFPAPAPASFPDPRLHYFCLYMHSHAGLH  
LHYGRDLSDKASLLCFQHEESLAQPPPLATSVTSMSPQNISLSPASFTFS  
FHSPPHTAHNASVDMCELRDQLLSQFLKHPQKASRSPASPAQOQSLSESLTS  
VRPMDWVSFEEDRIINATWKLQPTAGLQDLIHROEEOSEIMESVILERTLFOR  
TKGRGEAEKRLILVDFSSQALFODKNSOVAGEVYLGIVONTKVANITREPVLTFO  
HOLQKNTLVCOFVVEDPTLSPGHSAGCEYRRENOTSCPCNHLTYEPAVVS  
VEADVAHGHYLSLSYGVCSALACVSIAYILSRKRPRTYTKVMHLLAVFL  
DTSFLSEPVALTSEAGCRASAIPLHPSLTLCSMWGLSEGNLYRLVVEVGTYPG  
YLLKLSAMGWGPFLVTLVALVDVNDGPIILAVHRTPEGVYSPMCWIRDSLYI  
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## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 3564;  
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCGATGAGAT 21  
DB 228 TTCCGAGTTCGATGAGAT 208

## RESULT 38

AX061726 3686 bp DNA linear PAT 24-JUN-2001  
LOCUS AX061726  
DEFINITION Sequence 8 from Patent WO0100825.  
ACCESSION AX061726  
VERSION AX061726.1 GI:12539836

## SOURCE

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Dull, D. and Gorman, S.W.  
TITLE Human chromosome 15 and 16 bardet-biedl syndrome polynucleotides,  
polypeptides and methods of use  
JOURNAL Patent: WO 0100825-A 8 04-JUN-2001;  
CHIRON CORPORATION (US)

## FEATURES

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCGATGAGAT 21  
DB 318 TTCCGAGTTCGATGAGAT 298

## RESULT 39

BC008770/c 3702 bp mRNA linear PRI 29-JUN-2004  
LOCUS BC008770  
DEFINITION Homo sapiens G protein-coupled receptor 56, transcript variant 1,  
mRNA (cDNA clone MGC:11409 IMAGE:3139174), complete cds.  
ACCESSION BC008770  
VERSION BC008770.2 GI:33869362  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 3702)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diachenko, L., Marnett, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshynski, S.,  
Carrin, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mallya, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W.,  
Villalón, D.K., Kuzny, D.M., Sodergren, E.U., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Small, D.E.,  
Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

## TITLE

JOURNAL PUBMED  
2 (bases 1 to 3702)  
Strausberg, R.  
Direct Submission  
Submitted (25-MAY-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

## REFERENCE

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:14250619.  
Contact: MGC help desk  
Email: [cga@bbs-rcmail.nih.gov](mailto:cga@bbs-rcmail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@bbs.nih.gov](mailto:nisc.mgc@bbs.nih.gov)  
Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,  
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,  
Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

## REMARK

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRL Plate: 4 Row: 9 Column: 2  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 19923767.  
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/issue\_type="Placenta, choriochorionoma"  
/clone\_id="NIH\_MGC\_21"  
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159..2240

## FEATURES

source

## gene

## CDS

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/db_xref="LOCUSID:9289"
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VRPMGDMSFEEDRNATYKLOPTAGLDLHHSQRESEINERTYSLPRITFOR
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HQLQPNKNTLVCFWVEDPTLSPGHMSAGCEYVREKQPCGCRKRDYTIKVNML
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## ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 3702;  
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 344 TTCCGAGTCTCGATGAGAT 324

RESULT 40  
 CQ783397/c 3748 bp DNA linear PAT 17-MAR-2004  
 LOCUS CQ783397 Sequence 3537 from Patent EP1396543.  
 DEFINITION CQ783397  
 ACCESSION CQ783397  
 VERSION CQ783397.1 GI:45503325  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
 Koga, H.  
 Primers for synthesizing full length cDNA clones and their use  
 Patent: EP 1396543-A 3537 10-MAR-2004;  
 Research Association for Biotechnology (JP)  
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## CDS

ORIGIN  
 Query Match 95.5%; Score 21; DB 9; Length 3702;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 95.5%; Score 21; DB 6; Length 3748;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTCTCGATGAGAT 21  
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 430 TTCCGAGTCTCGATGAGAT 410

RESULT 41  
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 LOCUS BD127626 Primer for synthesizing full-length cDNA and use thereof.  
 DEFINITION BD127626  
 ACCESSION BD127626  
 VERSION BD127626.1 GI:23222571  
 KEYWORDS JP 2002017375-A/3057.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 3748)  
 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
 Koga, H.  
 Primers for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002017375-A 3057 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002017375-A/3057  
 PD 22-JAN-2002  
 PF 07-JUN-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO  
 PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI  
 SHINICHI KOJIMA,  
 PI TETSUJI OTSUKI, HISASHI KOGA  
 PC C12N15/09, C07K4/47, C07K6/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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 (245)..(2305).  
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## ORIGIN

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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTCTCGATGAGAT 21  
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 430 TTCCGAGTCTCGATGAGAT 410

RESULT 42  
 AK075270/c 3748 bp mRNA linear PRI 03-SEP-2002  
 LOCUS AK075270 Homo sapiens cDNA FLJ90789 f1s clone THYR01001523, highly similar  
 DEFINITION to Homo sapiens mRNA for TM7RN1 protein.  
 ACCESSION AK075270  
 VERSION AK075270.1 GI:22761246  
 KEYWORDS oligo capping; f1s (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1

## ORIGIN

**AUTHORS**  
 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuno, Y., Ota, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Nimomiya, K.

**TITLE**  
 NEDO human cDNA sequencing project

**JOURNAL**  
 Unpublished

**REFERENCE**  
 2 (bases 1 to 3748)  
 Isogai, T. and Otsuki, T.

**AUTHORS**  
 Direct Submission

**JOURNAL**  
 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert construction: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.).

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**Db**  
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**RESULT 43**  
 AX136371 3774 bp DNA linear PAT 30-MAY-2001  
 LOCUS AX136371  
 DEFINITION Sequence 293 from Patent EP1067182.  
 ACCESSION AX136371  
 VERSION AX136371.1 GI:14272777  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1  
 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.  
 Secretory protein or membrane protein  
 Patent: EP 1067182-A 293 10-JAN-2001;  
 Helix Research Institute (JP)  
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**AUTHORS**  
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**TITLE**  
 Secretory protein or membrane protein.

**JOURNAL**  
 Patent: JP 2002017376-A 147 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 3774;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 1 TTCCGAGTTCTCGATGAGAT 21  
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**Db**  
 453 TTCCGAGTTCTCGATGAGAT 433

**RESULT 45**  
 AK075555 3774 bp mRNA linear PRI 03-SEP-2002  
 LOCUS AK075555/c  
 DEFINITION Homo sapiens cDNA PSEC0255 file, clone NT2RBP3003536, highly similar  
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 ACCESSION AK075555  
 VERSION AK075555.1 GI:22761780

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 FH Key Location/Qualifiers  
 FT CDS (268)..(2328).

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 3774;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**Db**  
 453 TTCCGAGTTCTCGATGAGAT 433

**RESULT 45**  
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 LOCUS AK075555/c  
 DEFINITION Homo sapiens cDNA PSEC0255 file, clone NT2RBP3003536, highly similar  
 to Homo sapiens mRNA for TM7XN1 protein.  
 ACCESSION AK075555  
 VERSION AK075555.1 GI:22761780

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 FH Key Location/Qualifiers  
 FT CDS (268)..(2328).

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 3774;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
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**Db**  
 453 TTCCGAGTTCTCGATGAGAT 433

**RESULT 45**  
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 LOCUS AK075555/c  
 DEFINITION Homo sapiens cDNA PSEC0255 file, clone NT2RBP3003536, highly similar  
 to Homo sapiens mRNA for TM7XN1 protein.  
 ACCESSION AK075555  
 VERSION AK075555.1 GI:22761780

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 FH Key Location/Qualifiers  
 FT CDS (268)..(2328).

KEYWORDS oligo capping; fls (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Oca,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Satou,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahara,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3774)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) HRI human cDNA sequencing project; cDNA 5' - & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

source

1..3774

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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21

DB 453 TTCCGAGTTCTCGATGAGAT 433

RESULT 46

LOCUS CQ768015 3819 bp DNA linear PAT 04-MAR-2004

DEFINITION Sequence 482 from Patent EP1386931.

ACCESSION CQ768015

VERSION CQ768015.1 GI:45108767

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J. Human neurotrophin homologue Patent: EP 1386931-A 482 04-FEB-2004;

JOURNAL Genentech, Inc. (US)

FEATURES

source

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/db\_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21

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RESULT 47

LOCUS AX358880/c 3819 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 133 from Patent WO0193983.

ACCESSION AX358880

VERSION AX358880.1 GI:18675341

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0193983-A 133 13-DEC-2001;

JOURNAL Genentech Inc. (US)

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Best Local Similarity 100.0%; Pred. No. 41;

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RESULT 48

LOCUS AX362373 3819 bp DNA linear PAT 15-FEB-2002

DEFINITION Sequence 133 from Patent WO0208288.

ACCESSION AX362373

VERSION AX362373.1 GI:18694644

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I.

JOURNAL Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0208288-A 133 31-JAN-2002;

JOURNAL Genentech, Inc. (US)

FEATURES

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DB 399 TTCCGAGTTCTCGATGAGAT 379

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DEFINITION Sequence 91 from Patent WO0208284.
ACCESSION AX454506
VERSION AX454506.1 GI:21713877
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Maresters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 91 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Maresters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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399 TTGGAGTTCTCGATGAGAT 379
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RESULT 50
AX464272/c
LOCUS AX464272 3819 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 405 from Patent WO0140466.
ACCESSION AX464272
VERSION AX464272.1 GI:21899152
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 405 07-JUN-2001;
Genentech Inc. (US)
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/db_xref="taxon:9606"
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Query Match 95.5%; Score 21; DB 6; Length 3819;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 399 TTGGAGTTCTCGATGAGAT 379

Search completed: February 2, 2005, 00:37:47  
Job time : 1824 secs





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C 266	21	95.5	3819	10	ADH55887	ADH55887 Novel hum	C 339	21	95.5	3819	12	ADPF3800	ADPF3800 Human CDN
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C 268	21	95.5	3819	10	ADH64106	ADH64106 Novel hum	C 341	21	95.5	3819	12	ADPF27267	ADPF27267 Human CDN
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C 270	21	95.5	3819	10	ADH81416	ADH81416 Novel hum	C 343	21	95.5	3819	12	ADDE92294	ADDE92294 Novel hum
C 271	21	95.5	3819	10	ADH24055	ADH24055 Novel hum	C 344	21	95.5	3819	12	ADDE90595	ADDE90595 Human PRO
C 272	21	95.5	3819	10	ADG66907	ADG66907 CDNA enco	C 345	21	95.5	3819	12	ADPF41497	ADPF41497 Human CDN
C 273	21	95.5	3819	10	ADCD42825	ADCD42825 Novel hum	C 346	21	95.5	3819	12	ADPF31176	ADPF31176 Human CDN
C 274	21	95.5	3819	10	ADG68659	ADG68659 Novel hum	C 347	21	95.5	3819	12	ADPF25542	ADPF25542 Human CDN
C 275	21	95.5	3819	10	ADG67196	ADG67196 CDNA enco	C 348	21	95.5	3819	12	ADPF26643	ADPF26643 Human CDN
C 276	21	95.5	3819	10	ADG82585	ADG82585 Novel hum	C 349	21	95.5	3819	12	ADPF34432	ADPF34432 Human CDN
C 277	21	95.5	3819	10	ADN15984	ADN15984 Novel hum	C 350	21	95.5	3819	12	ADPF46669	ADPF46669 Human CDN
C 278	21	95.5	3819	10	ADN16613	ADN16613 Novel hum	C 351	21	95.5	3819	12	ADPF91742	ADPF91742 Novel hum
C 279	21	95.5	3819	10	ADN15432	ADN15432 Novel hum	C 352	21	95.5	3819	12	ADG05646	ADG05646 Human PRO
C 280	21	95.5	3819	10	ADN14880	ADN14880 Novel hum	C 353	21	95.5	3819	12	ADG27200	ADG27200 Human PRO
C 281	21	95.5	3819	10	ADG48836	ADG48836 Novel hum	C 354	21	95.5	3819	12	ADG02321	ADG02321 Human PRO
C 282	21	95.5	3819	10	ADG81142	ADG81142 Novel hum	C 355	21	95.5	3819	12	ADG22107	ADG22107 Novel hum
C 283	21	95.5	3819	10	ADG21007	ADG21007 Novel hum	C 356	21	95.5	3819	12	ADG20177	ADG20177 CDNA enco
C 284	21	95.5	3819	10	ADG05851	ADG05851 Human PRO	C 357	21	95.5	3819	12	ADPF98083	ADPF98083 Human PRO
C 285	21	95.5	3819	10	ADG76590	ADG76590 Human PRO	C 358	21	95.5	3819	12	ADG24300	ADG24300 Novel hum
C 286	21	95.5	3819	10	ADG75080	ADG75080 Human PRO	C 359	21	95.5	3819	12	ADPF98654	ADPF98654 Human PRO
C 287	21	95.5	3819	10	ADG75826	ADG75826 Novel hum	C 360	21	95.5	3819	12	ADG03485	ADG03485 Human PRO
C 288	21	95.5	3819	10	ADG85058	ADG85058 Novel hum	C 361	21	95.5	3819	12	ADPF99206	ADPF99206 Human PRO
C 289	21	95.5	3819	10	ADG86884	ADG86884 Novel hum	C 362	21	95.5	3819	12	ADG16791	ADG16791 CDNA enco
C 290	21	95.5	3819	10	ADG20761	ADG20761 Novel hum	C 363	21	95.5	3819	12	ADG05250	ADG05250 Human PRO
C 291	21	95.5	3819	10	ADG39058	ADG39058 Novel hum	C 364	21	95.5	3819	12	ADG19517	ADG19517 CDNA enco
C 292	21	95.5	3819	10	ADG87954	ADG87954 Human PRO	C 365	21	95.5	3819	12	ADG11263	ADG11263 CDNA enco
C 293	21	95.5	3819	10	ADG86358	ADG86358 Human PRO	C 366	21	95.5	3819	12	ADG13354	ADG13354 Novel hum
C 294	21	95.5	3819	10	ADG05605	ADG05605 Human PRO	C 367	21	95.5	3819	12	ADG08411	ADG08411 Human PRO
C 295	21	95.5	3819	10	ADG73590	ADG73590 Human PRO	C 368	21	95.5	3819	12	ADG15581	ADG15581 CDNA enco
C 296	21	95.5	3819	10	ADG75806	ADG75806 Human PRO	C 369	21	95.5	3819	12	ADG12042	ADG12042 Novel hum
C 297	21	95.5	3819	10	ADG48816	ADG48816 Human CDN	C 370	21	95.5	3819	12	ADPF6979	ADPF6979 Human PRO
C 298	21	95.5	3819	10	ADG78430	ADG78430 Novel hum	C 371	21	95.5	3819	12	ADG06164	ADG06164 Human PRO
C 299	21	95.5	3819	10	ADG41341	ADG41341 Human sec	C 372	21	95.5	3819	12	ADG23748	ADG23748 Novel hum
C 300	21	95.5	3819	10	ADG23382	ADG23382 CDNA enco	C 373	21	95.5	3819	12	ADG04037	ADG04037 Human PRO
C 301	21	95.5	3819	10	ADG21253	ADG21253 Novel hum	C 374	21	95.5	3819	12	ADG24938	ADG24938 Novel hum
C 302	21	95.5	3819	10	ADG77368	ADG77368 Novel hum	C 375	21	95.5	3819	12	ADPF94599	ADPF94599 Novel hum
C 303	21	95.5	3819	10	ADG20515	ADG20515 Novel hum	C 376	21	95.5	3819	12	ADG07235	ADG07235 Novel hum
C 304	21	95.5	3819	10	ADG75580	ADG75580 Human PRO	C 377	21	95.5	3819	12	ADG07787	ADG07787 Novel hum
C 305	21	95.5	3819	10	ADG74096	ADG74096 Human PRO	C 378	21	95.5	3819	12	ADG06695	ADG06695 Novel hum
C 306	21	95.5	3819	10	ADG74342	ADG74342 Human PRO	C 379	21	95.5	3819	12	ADG55282	ADG55282 Novel hum
C 307	21	95.5	3819	10	ADG76072	ADG76072 Novel hum	C 380	21	95.5	3819	12	ADG60946	ADG60946 Novel hum
C 308	21	95.5	3819	10	ADG85564	ADG85564 Novel hum	C 381	21	95.5	3819	12	ADG62050	ADG62050 Novel hum
C 309	21	95.5	3819	10	ADG23934	ADG23934 CDNA enco	C 382	21	95.5	3819	12	ADG62251	ADG62251 Human PRO
C 310	21	95.5	3819	10	ADG24577	ADG24577 CDNA enco	C 383	21	95.5	3819	12	ADG57490	ADG57490 Novel hum
C 311	21	95.5	3819	10	ADG87402	ADG87402 Human PRO	C 384	21	95.5	3819	12	ADG55638	ADG55638 Novel hum
C 312	21	95.5	3819	10	ADG05113	ADG05113 Human PRO	C 385	21	95.5	3819	12	ADG55834	ADG55834 Novel hum
C 313	21	95.5	3819	10	ADG75326	ADG75326 Human PRO	C 386	21	95.5	3819	12	ADG55834	ADG55834 Novel hum

C 387	21	95.5	3819	12	ADG58594	ADG58594	Novel	hum	hum	C 460	16.8	76.4	1238	10	ABQ80357	Abq80357 A. fumig
C 388	21	95.5	3819	12	ADG70960	ADG70960	Novel	hum	hum	C 461	16.8	76.4	1504	3	AACT79921	AACT79921 Human sec
C 389	21	95.5	3819	12	ADH39039	ADH39039	Novel	hum	hum	C 462	16.8	76.4	6535	12	ADN06015	ADN06015 Antipsoi
C 390	21	95.5	3819	12	ADG58042	ADG58042	Novel	hum	hum	C 463	16.4	74.5	431	1	AACT6998	AACT6998 Arabidops
C 391	21	95.5	3819	12	ADG53626	ADG53626	Novel	hum	hum	C 464	16.4	74.5	441	11	ABD11444	ABD11444 Pseudomon
C 392	21	95.5	3819	12	ADG71512	ADG71512	Novel	hum	hum	C 465	16.4	74.5	703	10	ADKS8302	ADKS8302 Plant DNA
C 393	21	95.5	3819	12	ADG50655	ADG50655	Novel	hum	hum	C 466	16.4	74.5	1659	11	ABD11857	ABD11857 Pseudomon
C 394	21	95.5	3819	12	ADG81699	ADG81699	Novel	hum	hum	C 467	16.4	74.5	3222	8	ACA42673	ACA42673 Prokaryot
C 395	21	95.5	3819	12	ADH30661	ADH30661	Novel	PRO	PRO	C 468	16.4	74.5	3267	11	ABD12103	ABD12103 Pseudomon
C 396	21	95.5	3819	12	ADH12028	ADH12028	Novel	hum	hum	C 469	16.4	74.5	3768	8	ABX11869	ABX11869 Sindbis p
C 397	21	95.5	3819	12	ADG51003	ADG51003	Novel	CDN	CDN	C 470	16.2	73.6	168	6	ABN16138	ABN16138 Human ORF
C 398	21	95.5	3819	12	ADG51903	ADG51903	Novel	CDN	CDN	C 471	16.2	73.6	461	9	ACH48110	ACH48110 Human lun
C 399	21	95.5	3819	12	ADG52450	ADG52450	Novel	hum	hum	C 472	16.2	73.6	467	6	ABV72644	ABV72644 Human his
C 400	21	95.5	3819	12	ADG54178	ADG54178	Novel	hum	hum	C 473	16.2	73.6	484	9	ACH30178	ACH30178 Human tes
C 401	21	95.5	3819	12	ADG49407	ADG49407	Novel	CDN	CDN	C 474	16.2	73.6	519	11	ABD15884	ABD15884 Pseudomon
C 402	21	95.5	3819	12	ADG81147	ADG81147	Novel	PRO	PRO	C 475	16.2	73.6	520	5	AAH87842	AAH87842 Peppermi
C 403	21	95.5	3819	12	ADG56386	ADG56386	Novel	hum	hum	C 476	16.2	73.6	534	8	ACA52981	ACA52981 Prokaryot
C 404	21	95.5	3819	12	ADH12652	ADH12652	Novel	hum	hum	C 477	16.2	73.6	568	6	ABQ42457	ABQ42457 Oligonuc
C 405	21	95.5	3819	12	ADG48783	ADG48783	Novel	CDN	CDN	C 478	16.2	73.6	622	5	AAH87833	AAH87833 Oligonuc
C 406	21	95.5	3819	12	ADG61498	ADG61498	Novel	hum	hum	C 479	16.2	73.6	644	10	ADKS6807	ADKS6807 Plant DNA
C 407	21	95.5	3819	12	ADH28585	ADH28585	Novel	PRO	PRO	C 480	16.2	73.6	649	3	AAFI2142	AAFI2142 Aspergill
C 408	21	95.5	3819	12	ADG54320	ADG54320	Novel	hum	hum	C 481	16.2	73.6	927	8	ABT21167	ABT21167 Aspergill
C 409	21	95.5	3819	12	ADG59770	ADG59770	Novel	hum	hum	C 482	16.2	73.6	933	8	ABT19347	ABT19347 Oligonuc
C 410	21	95.5	3819	12	ADG51279	ADG51279	Novel	CDN	CDN	C 483	16.2	73.6	933	8	ABT19347	ABT19347 Oligonuc
C 411	21	95.5	3819	12	ADH43524	ADH43524	Novel	PRO	PRO	C 484	16.2	73.6	977	6	ABQ25057	ABQ25057 Oligonuc
C 412	21	95.5	3819	12	ADG59923	ADG59923	Novel	CDN	CDN	C 485	16.2	73.6	982	6	ABQ24918	ABQ24918

PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX WPI; 2003-689676/65.  
 DR  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Claim 4; Page 125; 129pp; English.  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytotactic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence represents a GPR56 antisense  
 CC probe from the present invention.  
 CC  
 SQ Sequence 22 BP; 4 A; 4 C; 7 G; 7 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 22; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Gaps 0;  
 Matches 22; Conservative 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGATC 22  
 DB 1 TTGGAGTTCTCGATGAGATC 22  
 RESULT 2  
 ADA14227/c  
 ID ADA14227 standard; DNA; 22 BP.  
 XX  
 AC ADA14227;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE GPR56 sense probe SEQ ID NO:11.  
 XX  
 KW human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KW GPR56; cancer; ovarian cancer; metastasis; tumour; cytotactic;  
 KW gene therapy; probe; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003068965-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 12-FEB-2003; 2003WO-AU000178.  
 XX  
 PR 12-FEB-2002; 2002US-00073054.  
 XX  
 PA (GTWO-) G2 THERAPIES LTD.  
 XX  
 PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX  
 DR WPI; 2003-689676/65.  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Claim 2; Page 124; 129pp; English.

XX  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytotactic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence represents a GPR56 sense  
 CC probe from the present invention.  
 CC  
 SQ Sequence 22 BP; 7 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Gaps 0;  
 Matches 21; Conservative 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 DB 22 TTGGAGTTCTCGATGAGAT 22  
 RESULT 3  
 AAX41171/c  
 ID AAX41171 standard; cDNA; 372 BP.  
 XX  
 AC AAX41171;  
 XX  
 DT 17-JUN-1999 (first entry)  
 XX  
 DE Human secreted protein 5' EST SEQ ID NO:115.  
 XX  
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;  
 KW forensic; gene therapy; chromosome mapping; signal peptide;  
 KW upstream regulatory sequence; cytokine activity; cell proliferation;  
 KW differentiation; haematopoiesis regulation; tissue growth regulation;  
 KW reproductive hormone regulation; chemokine; chemokine; haemostatic;  
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9906548-A2.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 31-JUL-1998; 98WO-IB001222.  
 XX  
 PR 01-AUG-1997; 97US-00905135.  
 XX  
 PA (BEST) GENSET.  
 XX  
 PI Dunas Milne Edwards J, Duclert A, Lacroix B;  
 XX  
 DR WPI; 1999-153778/13.  
 XX  
 DR P-PSDB; AAY12338.  
 XX  
 PT New nucleic acids encoding human secreted proteins - obtained from cDNA  
 PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,  
 PT umbilical cord, placenta and colon tissue.  
 XX  
 PS Claim 1; Page 274; 824pp; English.  
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for  
 CC human secreted proteins, and encode the proteins given in AAY12261 to  
 CC AAY12514, respectively. The proteins given represent the signal peptide  
 CC and an N-terminal fragment of a secreted protein. The nucleic acid  
 CC sequences can be used for producing secreted human gene products. They

CC can also be used to develop products for diagnosis and therapy. The  
 CC proteins obtained may have cytokine activity, cell  
 CC proliferation/differentiation activity, hematopoietic regulating  
 CC activity, tissue growth regulating activity, reproductive hormone  
 CC regulating activity, chemokine/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, tumour inhibition activity or other activities. The products  
 CC can be used in forensic, gene therapy and chromosome mapping procedures.  
 CC The sequences can also be used for obtaining corresponding promoter  
 CC sequences. The nucleic acids encoding the signal peptide can be used for  
 CC directing extracellular secretion of a polypeptide or the insertion of a  
 CC polypeptide into a membrane, or importing a polypeptide into a cell  
 XX

SO Sequence 372 BP; 92 A; 115 C; 104 G; 55 T; 0 U; 6 Other;

Query Match 95.5%; Score 21; DB 2; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 369 TTCGAGTTCTCGATGAGAT 349

RESULT 4  
 AAI27155/c  
 ID AAI27155 standard; DNA; 423 BP.  
 XX  
 AC AAI27155;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Probe #17088 for gene expression analysis in human cervical cell sample.  
 KM Probe: human; microarray; gene expression; cervical epithelial cell;  
 KM cervical cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200157278-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488901/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human cervical epithelial cells.  
 XX  
 PS Claim 25; SEQ ID NO 17088; 487DP; English.  
 XX  
 CC The present invention relates to human single exon nucleic acid probes  
 CC (SNP). The present sequence is one such probe. The SNPs are derived  
 CC from human HeLa cells. The SNPs can be used to produce a single exon  
 CC microarray, which can be used for measuring human gene expression in a  
 CC sample derived from human cervical epithelial cells. By measuring gene  
 CC expression, the probes are therefore useful in grading and/or staging of  
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SO Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 122 TTCGAGTTCTCGATGAGAT 102

RESULT 5  
 ABA75435/c  
 ID ABA75435 standard; DNA; 423 BP.  
 XX  
 AC ABA75435;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human foetal liver single exon nucleic acid probe #23740.  
 KM Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human fetal liver.  
 XX  
 PS Claim 4; SEQ ID NO 23740; 639P + Sequence Listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SO Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 122 TTCGAGTTCTCGATGAGAT 102

RESULT 6

AA156007/c  
ID AA156007 standard; DNA; 423 BP.  
XX  
AC AA156007;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Probe #24693 used to measure gene expression in human placenta sample.  
XX  
KM Probe; microarray; human; placenta; antenatal diagnosis;  
KM genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 25; SEQ ID NO 24693; 654pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX  
SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
XX  
Query Match 95.5%; Score 21; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TTCGAGTTCGATGAGAT 21  
DB 122 TTCGAGTTCGATGAGAT 102  
XX  
RESULT 7  
ABA40063/c  
ID ABA40063 standard; DNA; 423 BP.  
XX  
AC ABA40063;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
PF Probe #18529 for gene expression analysis in human heart cell sample.  
XX  
KM Human; gene expression; heart; microarray; vascular system; probe;  
KM cardiovascular disease; hypertension; cardiac arrhythmia;  
KM congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.

XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000666.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX  
PS Claim 4; SEQ ID NO 18529; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
XX  
Query Match 95.5%; Score 21; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TTCGAGTTCGATGAGAT 21  
DB 122 TTCGAGTTCGATGAGAT 102  
XX  
RESULT 8  
AAK50067/c  
ID AAK50067 standard; DNA; 423 BP.  
XX  
AC AAK50067;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 24624.  
XX  
KM Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000668.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.



```

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488900/53.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 24624; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGAGTTCGATGAGAT 21
Db 122 TTCCGAGTTCGATGAGAT 102
XX
XX RESULT 9
XX ID AAK24002/c
XX AAK24002 standard; DNA; 423 BP.
XX
XX AAK24002;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 23993.
XX
XX Human brain expressed exon; gene expression analysis; probe; microarray;
KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KM sb.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-483446/52.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brain.
XX
XX Example 4; SEQ ID NO 23993; 650bp + Sequence Listing; English.
XX

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CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGAGTTCGATGAGAT 21
Db 122 TTCCGAGTTCGATGAGAT 102
XX
XX RESULT 10
XX ID ABS49706/c
XX ABS49706 standard; DNA; 423 BP.
XX
XX ABS49706;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver single exon probe, SEQ ID NO 24696.
XX
XX Human single exon nucleic acid probe; liver; cirrhosis;
KM hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KM coronary heart disease; sb.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488898/53.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 24696; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SNP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 1109 defined nucleotide sequences given in the
CC specification (or complements/fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (1) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
 SQ  
 Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCGATGAGAT 21  
 DB 122 TTGGAGTTCGATGAGAT 102  
 RESULT 11  
 ABS23554/C  
 ID ABS23554 standard; DNA; 423 BP.  
 AC ABS23554;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 23545.  
 XX  
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease; open reading frame; ORF.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-PEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-0063236P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 PS  
 PS Claim 4; SEQ ID NO 23545; 634bp; English.  
 CC  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridise at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA; and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene.  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
 XX  
 Query Match 95.5%; Score 21; DB 6; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCGATGAGAT 21  
 DB 122 TTGGAGTTCGATGAGAT 102  
 RESULT 12  
 ADL40560/C  
 ID ADL40560 standard; DNA; 493 BP.  
 XX  
 AC ADL40560;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human ovarian cancer DNA marker #14450.  
 XX  
 KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200170979-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US009126.  
 XX  
 PR 21-MAR-2000; 2000US-0191031P.  
 PR 25-MAY-2000; 2000US-0207124P.  
 PR 15-JUN-2000; 2000US-0211940P.  
 PR 07-JUL-2000; 2000US-0216820P.  
 PR 25-JUL-2000; 2000US-0220661P.  
 PR 21-DEC-2000; 2000US-0257672P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Lee J, Lillie J;  
 XX  
 DR WPI; 2001-611502/70.  
 XX  
 PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian  
 PT cancer cells as compared to their normal non-cancerous ovarian cells are  
 PT used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 14450; 106bp; English.  
PS  
XX The invention relates to nucleic acid markers which are overexpressed in  
CC ovarian cancer cells as compared to their expression in normal (i.e. non-  
CC cancerous) ovarian cells. The invention also relates to polypeptides  
CC encoded by the markers, antibodies that selectively bind to the  
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk  
CC of developing ovarian cancer involving inhibiting expression of a gene  
CC corresponding to a marker of the invention and a method of treating a  
CC patient afflicted with ovarian cancer comprising providing to cells of  
CC the patient an antisense oligonucleotide complementary to a marker of the  
CC invention. The markers are useful for assessing if a patient is afflicted  
CC with ovarian cancer, which involves comparing the level of expression of  
CC a marker in a patient sample and a normal level of expression of the  
CC marker in a control non-ovarian cancer sample. A difference between the  
CC expression levels indicates ovarian cancer. The level of expression of a  
CC marker corresponds to a secreted protein or to a transcribed  
CC polynucleotide or its portion. The level of expression of the marker is  
CC assessed by detecting the presence in the sample, a protein or protein  
CC fragment corresponding to the marker. The presence of protein or protein  
CC fragment is detected using an antibody that specifically binds with the  
CC protein or protein fragment. Alternatively, the level of expression of  
CC the marker is assessed by detecting the presence of a transcribed  
CC polynucleotide which anneals with the marker or anneals with a portion of  
CC the polynucleotide comprising the marker, under stringent conditions. The  
CC marker is also used for monitoring the progression of ovarian cancer in a  
CC patient which involves detecting expression of the marker in a patient  
CC sample at a first point in time, repeating the method at a subsequent  
CC time and comparing the level of expression. The method is carried out  
CC using an ovarian tissue sample. A composition comprising a marker,  
CC polypeptide or antibody of the invention is used to treat ovarian cancer.  
CC This sequence represents a human ovarian cancer DNA marker of the  
CC invention.  
XX  
SQ Sequence 493 BP; 93 A; 171 C; 130 G; 99 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 5; Length 493;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCGATGGAGAT 21  
Db 416 TTGGAGTTCGATGGAGAT 396  
RESULT 13  
ADQ20571/c  
ID ADQ20571 standard; DNA; 527 BP.  
XX  
XX ADQ20571;  
AC  
XX  
XX 26-AUG-2004 (first entry)  
DT  
XX  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3391.  
XX  
XX soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human;  
KW ds.  
XX  
XX Homo sapiens.  
OS  
XX WO2004048938-A2.  
PN  
XX 10-JUN-2004.  
PD  
XX 26-NOV-2003; 2003WO-US038193.  
PF  
XX 26-NOV-2002; 2002US-0429739P.  
PR  
XX (PROT-) PROTEIN DESIGN LABS INC.  
PA  
XX Aziz N, Ginsburg WM, Zlotnick A;  
PI  
XX

DR WPI; 2004-441208/41.  
XX  
XX Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.  
XX  
XX Example 2; SEQ ID NO 3391; 210bp; English.  
PS  
XX The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in the first soft tissue sample, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytoskeletal applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.  
XX  
SQ Sequence 527 BP; 106 A; 186 C; 128 G; 107 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 12; Length 527;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCGATGGAGAT 21  
Db 247 TTGGAGTTCGATGGAGAT 227  
RESULT 14  
AA118016/c  
ID AA118016 standard; DNA; 582 BP.  
XX  
XX AA118016;  
AC  
XX  
XX 12-OCT-2001 (first entry)  
DT  
XX  
DE Probe #7949 for gene expression analysis in human cervical cell sample.  
XX  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157278-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488901/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.  
PT  
XX Claim 25; SEQ ID NO 7949; 487bp; English.  
PS

XX The present invention relates to human single exon nucleic acid probes  
 CC (SNP). The present sequence is one such probe. The SNPs are derived  
 CC from human HeLa cells. The SNPs can be used to produce a single exon  
 CC microarray, which can be used for measuring human gene expression in a  
 CC sample derived from human cervical epithelial cells. By measuring gene  
 CC expression, the probes are therefore useful in grading and/or staging of  
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21

DB 227 TTCGAGTTCTCGATGAGAT 207

RESULT 15

ABA62983/C

ID ABA62983 standard; DNA; 582 BP.

AC ABA62983;

DT 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #11288.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000669.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

XX Claim 1; SEQ ID NO 11288; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21

DB 227 TTCGAGTTCTCGATGAGAT 207

RESULT 16

AA143010/C

ID AA143010 standard; DNA; 582 BP.

AC AA143010;

DT 17-OCT-2001 (first entry)

XX Probe #11696 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 11696; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SNP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21

DB 227 TTCGAGTTCTCGATGAGAT 207

RESULT 17

ABA30246/C

ID ABA30246 standard; DNA; 582 BP.

AC ABA30246;

XX 23-JAN-2002 (first entry)

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XX DE Probe #8712 for gene expression analysis in human heart cell sample.
XX XX
XX KM Human; gene expression; heart; microarray; vascular system; probe;
XX KM cardiovascular disease; hypertension; cardiac arrhythmia;
XX KM congenital heart disease; ss.
XX OS Homo sapiens.
XX XX MO200157274-A2.
XX PN
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-48899/53.
XX DR
XX XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 1; SEQ ID NO 8712; 530bp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 4; Length 582;
XX Best Local Similarity 100.0%; Pred. No. 5.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGAGTTCTCGATGAGAT 21
XX Db 227 TTGCGAGTTCTCGATGAGAT 207
XX
XX RESULT 18
XX ID AAK37182/c
XX ID AAK37182 standard; DNA; 582 BP.
XX XX
XX AC AAK37182;
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 11739.
XX XX
XX KM Human; bone marrow expressed exon; gene expression analysis; probe;
XX KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX XX
XX PN MO200157276-A2.

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XX XX
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-48899/53.
XX DR
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX XX
XX PS Example 4; SEQ ID NO 11739; 658bp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX CC the probes of the invention
XX CC
XX SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 4; Length 582;
XX Best Local Similarity 100.0%; Pred. No. 5.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGAGTTCTCGATGAGAT 21
XX Db 227 TTGCGAGTTCTCGATGAGAT 207
XX
XX RESULT 19
XX ID AAK11396/c
XX ID AAK11396 standard; DNA; 582 BP.
XX XX
XX AC AAK11396;
XX DT 05-NOV-2001 (first entry)
XX XX
XX DE Human brain expressed single exon probe SEQ ID NO: 11387.
XX XX
XX KM Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KM ss.
XX OS Homo sapiens.
XX XX
XX PN MO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.

```

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI, 2001-483446/52.  
 DR Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains.  
 PT Example 4; SEQ ID NO 11887; 650bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 XX  
 SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCGATGAGAT 21  
 DB 227 TTCGAGTTCGATGAGAT 207  
 RESULT 20  
 ABS36856/C  
 ID ABS36856 standard; DNA; 582 BP.  
 XX  
 AC ABS36856;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human liver single exon probe, SEQ ID NO 11846.  
 XX  
 DE Human single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI, 2001-488898/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human adult liver.  
 PS Claim 1; SEQ ID NO 11846; 658bp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (I) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
 CC liver single exon nucleic acid probes of the invention. Note: The  
 CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pat\_sequences  
 XX  
 SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCGATGAGAT 21  
 DB 227 TTCGAGTTCGATGAGAT 207  
 RESULT 21  
 ABS11174/C  
 ID ABS11174 standard; DNA; 582 BP.  
 XX  
 AC ABS11174;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe from lung SEQ ID NO 11165.  
 XX  
 DE Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI, 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 XX measure gene expression in human lung samples.  
 PS Claim 1; SEQ ID NO 11165; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC collected from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC histadactylosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 6; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
 |||||

DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 22

XX ID AAK92315/c

XX ID AAK92315 standard; cDNA; 739 BP.

XX AAK92315;

XX 06-NOV-2001 (first entry)

XX Human cDNA 5'-end sequence, SEQ ID NO: 775.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.

XX Claim 2; SEQ ID NO 775; 1380bp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is the nucleotide sequence of the 5'-end of  
 CC a cDNA provided in the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in CD-  
 CC ROM format directly from EPO

XX SQ Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 739;

XX Best Local Similarity 100.0%; Pred. No. 5.3;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
 |||||

DB 430 TTGGAGTTCTCGATGAGAT 410

RESULT 23

XX ID AAK93857/c

XX ID AAK93857 standard; cDNA; 739 BP.

XX AAK93857;

XX 06-NOV-2001 (first entry)

XX Human cDNA clone representative sequence, SEQ ID NO: 2317.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.

XX 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.

XX Example 11; SEQ ID NO 2317; 1380bp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have



CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesized by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence was used as the representative sequence  
 CC from a human clone which was used in homology searches to identify the  
 CC clone. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in CD-ROM format directly from  
 CC EPO

XX Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

Query Match 95.5%; Score 21; DB 4; Length 739;

Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 24

ADL28742/C  
 ID ADL28742 standard; cDNA; 739 BP.

XX ADL28742;

XX 20-MAY-2004 (first entry)

XX 5' end of a human cDNA molecule Segid 775.

XX human; medicine; signal transduction; glycoprotein; transcription;

KW oligo-capping method; ss.

XX Homo sapiens.

XX EPI396543-A2.

XX 10-MAR-2004.

XX 07-JUL-2000; 2003EP-00025638.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-0018774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2004-204755/20.

PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
 length human cDNAs.

XX Disclosure; SEQ ID NO 775; 1340BP; English.

XX This invention relates to a novel primers useful for synthesizing full  
 CC length cDNA molecules that encode human proteins. Specifically, it refers  
 CC to secretory or membrane proteins that are potential therapeutic agents/  
 CC target molecules in the field of medicine, and in particular genes  
 CC encoding proteins that are associated with signal transduction,  
 CC glycoproteins and transcription. The present invention describes a method  
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
 CC ends using the oligo-capping method. This polynucleotide sequence is the  
 CC 5' end of a full length human cDNA sequence of the invention.

XX Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

Query Match 95.5%; Score 21; DB 12; Length 739;

Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 25

ADL30284/C  
 ID ADL30284 standard; cDNA; 739 BP.

XX ADL30284;

XX 20-MAY-2004 (first entry)

XX 3' end of a representative human cDNA cluster Segid 2317.

XX human; medicine; signal transduction; glycoprotein; transcription;

KW oligo-capping method; ss.

XX Homo sapiens.

XX EPI396543-A2.

XX 10-MAR-2004.

XX 07-JUL-2000; 2003EP-00025638.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-0018774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2004-204755/20.

PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
 length human cDNAs.

XX Example 18; SEQ ID NO 2317; 1340BP; English.

XX This invention relates to a novel primers useful for synthesizing full  
 CC length cDNA molecules that encode human proteins. Specifically, it refers  
 CC to secretory or membrane proteins that are potential therapeutic agents/  
 CC target molecules in the field of medicine, and in particular genes  
 CC encoding proteins that are associated with signal transduction,  
 CC glycoproteins and transcription. The present invention describes a method  
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
 CC ends using the oligo-capping method. This polynucleotide sequence is the  
 CC 3' end of a representative human cDNA cluster of the invention.

XX Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

Query Match 95.5%; Score 21; DB 12; Length 739;

Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 26

AAF94095/C  
 ID AAF94095 standard; DNA; 745 BP.

XX AAF94095;

DT 23-MAY-2001 (first entry)  
XX  
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 529.  
XX  
KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
KW rheumatoid arthritis; diabetes; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN EP1067182-A2.  
XX  
PD 10-JAN-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114090.  
XX  
PR 08-JUL-1999; 99JP-00194179.  
PR 11-JAN-2000; 2000JP-00118775.  
PR 02-MAY-2000; 2000JP-00183766.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Oka T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX  
DR WPI; 2001-033989/11.  
XX  
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
PT gene therapy or as candidate target molecules in drug development.  
XX  
PS Claim 4; SEQ ID NO 529; 609p + Sequence Listing; English.  
XX  
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by AAB88317  
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
CC invention. The invention also includes methods for the production of  
CC antibodies directed against the proteins, and cDNA sequences, which can  
CC be used in vaccines. The polynucleotide sequences can be used in gene  
CC therapy. The polynucleotide sequences and the proteins they encode may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate secretory protein/membrane protein expression. The  
CC nucleic acids and complementary sequences may also be used as DNA probes  
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
CC and quantitate the presence of similar nucleic acid sequences in samples.  
CC They may also be used to study the expression and function of secretory  
CC proteins/membrane polypeptides and their role in metabolism. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC against them and in assays to identify modulators (agonists and  
CC antagonists) of expression and activity. The antibodies and antagonists  
CC may also be used as therapeutic agents to down regulate expression and  
CC activity. The antibodies may also be used as diagnostic agents for  
CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA). Examples of diseases which may be  
CC treated include rheumatoid arthritis and diabetes  
XX  
XX Sequence 745 BP; 143 A; 251 C; 194 G; 154 T; 0 U; 3 Other;  
XX  
Query Match 95.5%; Score 21; DB 5; Length 745;  
Best Local Similarity 100.0%; Pred. No. 5.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGAGTTCGATGAGAT 21  
DB 453 TTCCGAGTTCGATGAGAT 433  
RESULT 27  
ADA09908/c  
ID ADA09908 standard; cDNA; 1142 BP.  
XX  
AC ADA09908;  
XX  
DT 20-NOV-2003 (first entry)  
XX

DE Human receptor and membrane-associated protein REMAP-12 cDNA, SEQ ID:50.  
XX  
XX Human; receptor and membrane-associated protein; REMAP;  
KW cell proliferative disorder; cancer; autoimmune disorder;  
KW inflammatory disorder; infection; neurological disorder;  
KW metabolic disorder; developmental disorder; endocrine disorder;  
KW cytostatic; immunosuppressive; antiinflammatory; neuroprotective;  
KW neurotropic; cerebroprotective; gene therapy;  
KW single nucleotide polymorphism; SNP; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key  
XX CDS  
XX  
XX Location/Qualifiers  
XX 96..554  
XX /\*tag= a  
XX /product= "REMAP-12"  
XX /replace(109,T)  
XX /\*tag= b  
XX  
XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(112,C)  
XX /\*tag= c  
XX /note= "Single nucleotide polymorphism (SNP); results in  
XX L6P substitution in the encoded protein"  
XX /replace(117,T)  
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XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(571,C)  
XX /\*tag= e  
XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(573,C)  
XX /\*tag= f  
XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(574,C)  
XX /\*tag= g  
XX /note= "Single nucleotide polymorphism (SNP)"  
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XX /\*tag= h  
XX /note= "Single nucleotide polymorphism (SNP)"  
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XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(694,G)  
XX /\*tag= j  
XX /note= "Single nucleotide polymorphism (SNP)"  
XX /replace(696,G)  
XX /\*tag= k  
XX /note= "Single nucleotide polymorphism (SNP)"  
XX  
XX WO2003070902-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 18-FEB-2003; 2003WO-US004902.  
XX  
XX  
XX 20-FEB-2002; 2002US-0358279P.  
XX 13-MAR-2002; 2002US-0364338P.  
XX 25-APR-2002; 2002US-0375657P.  
XX 29-APR-2002; 2002US-0376669P.  
XX 10-MAY-2002; 2002US-0379837P.  
XX 10-MAY-2002; 2002US-0379853P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX

PI Chawla NK, Yue H, Richardson TW, Marquis JP, Lehr-Mason PM;  
PI Goryad AE, Becha SD, Kable AE, Swarnakar A, Jin P, Hawkins PR;  
PI Chien D, Ramkumar J, Tran UK, Hafajia AJA, Baughn MR, Lee SY;  
PI Jiang X, Jackson AH, Khare R, Bullock SA;  
XX  
XX WPI; 2003-697610/66.  
DR P-PSDB; ADA09870.  
XX  
XX New human receptor and membrane associated proteins and nucleic acids,  
PT useful for diagnosing, treating or preventing e.g. viral, bacterial,  
PT fungal, parasitic, protozoan or helminthic infections, cancers,  
PT neurological disorders.  
XX  
XX Claim 5; Page 276; 298pp; English.  
PS  
XX The invention relates to 38 human receptors and membrane-associated  
CC proteins (REMAP), REMAP-1 to REMAP-38, and the cDNAs encoding them  
CC (ADA09859-ADA09934). The invention also encompasses expression  
CC constructs, host cells and transgenic organisms comprising a REMAP  
CC nucleic acid sequence; the recombinant preparation of a REMAP; an  
CC antibody against a REMAP; methods of detection of REMAP proteins or  
CC nucleic acids; a micro-array containing REMAP nucleic acids; methods of  
CC screening compounds for their ability to modulate REMAP activity or  
CC expression; and pharmaceutical compositions comprising a REMAP protein, a  
CC REMAP agonist or REMAP antagonist. The REMAP proteins, nucleic acids or  
CC compositions comprising them are useful in diagnosing, treating or  
CC preventing a variety of disorders, including cell proliferative disorders  
CC (e.g., arteriosclerosis, cirrhosis, hepatitis, psoriasis, or primary  
CC thrombocytopenia) or cancers (e.g., adenocarcinoma, leukemia, or cancers  
CC of the bone, brain, breast or uterus); autoimmune/inflammatory disorders  
CC (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple  
CC sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus  
CC erythematosus); viral, bacterial, fungal, parasitic, protozoan or  
CC helminthic infections; neurological disorders (e.g., epilepsy, stroke,  
CC Alzheimer's disease, dementia, or Parkinson's disease); metabolic  
CC disorders (e.g., hereditary fructose intolerance, obesity, hypoglycaemia  
CC or diabetes); developmental disorders (e.g., achondroplastic dwarfism,  
CC hypothyroidism or hydrocephalus); or endocrine disorders (e.g., disorders  
CC of the hypothalamus or pituitary gland). The present sequence represents  
CC a REMAP cDNA of the invention. Note: Additional single nucleotide  
CC polymorphisms (SNPs) are given for this sequence at positions 193, 572,  
CC 625 and 693; however, for each of these, neither variant disclosed  
CC matches the nucleotide given in the sequence.  
XX  
SQ Sequence 1142 BP; 269 A; 343 C; 281 G; 249 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 9; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
DB 281 TTCGAGTCTCGATGAGAT 261  
|||||  
|||||

RESULT 28  
AA35742/c  
ID AA35742 standard; cDNA; 2061 BP.  
XX  
XX AA35742;  
XX  
XX 09-JUL-1999 (first entry)  
XX  
XX cDNA encoding a protein identified by the signal sequence trap method.  
DE  
XX Signal sequence trap method; SST method; immunisation; inhibition;  
XX infection; allergy; cancer; regulation; tissue formation; tissue repair;  
XX activin activity; inhibin activity; chemokine activity;  
XX cytokine activity; blood coagulation regulation; agonist; antagonist;  
XX metabolic disorder; hormonal disorder; immune disorder;  
XX severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;  
XX  
XX 88.

OS Homo sapiens.  
XX  
XX MO9918126-A1.  
XX  
XX 15-APR-1999.  
XX  
XX  
XX 06-OCT-1998; 98WO-JP004514.  
XX  
XX 07-OCT-1997; 97JP-00274674.  
XX  
XX (ONOR) ONO PHARM CO LTD.  
XX  
XX Fukushima D, Shibayama S, Tada H;  
PI  
XX WPI; 1999-277254/23.  
DR P-PSDB; AA02382.  
XX  
XX Polypeptides identified by the signal sequence trap method from a human  
PT cDNA library.  
XX  
XX Claim 4; Page 231-232; 281pp; Japanese.  
PS  
XX AA35694-X35747 represent cDNA sequences that encode novel polypeptides  
CC (AA02358-84) which are identified from a human placental cDNA library by  
CC the signal sequence trap (SST) method. The polypeptides have a broad  
CC range of physiological activity, including immunisation against and  
CC inhibition of infections, allergies and cancer; regulation of tissue  
CC formation and repair; activin/inhibin activity; chemokine/cytokine  
CC activity; blood coagulation regulation; and receptor/ligand agonist or  
CC antagonist activity. The polypeptides can be used for prevention and  
CC treatment of disorders including infections by bacteria, yeasts and  
CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;  
CC immune disorders (including severe combined immunodeficiency (SCID) and  
CC AIDS; thrombosis; cancer; and traumatic or surgical wounds  
XX  
SQ Sequence 2061 BP; 384 A; 699 C; 541 G; 437 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 2; Length 2061;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
DB 186 TTCGAGTCTCGATGAGAT 166  
|||||  
|||||

RESULT 29  
ADO29927/c  
ID ADO29927 standard; cDNA; 2064 BP.  
XX  
XX ADO29927;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Human GPCR GPR56 polynucleotide, SEQ ID NO:1029.  
DE  
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
XX transgenic mouse; neurological disorder; adrenal gland disorder;  
XX colon disorder; intestinal disorder; cardiovascular disorder;  
XX muscular disorder; blood disorder; immune disorder; bone disorder;  
XX joint disorder; metabolic disorder; nutritive disorder; cancer;  
XX kidney disorder; liver disorder; lung disorder; breast disorder;  
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;  
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
XX thymus disorder; thyroid disorder; antiparinsonian; anti-manic;  
XX cytoskeletal; anti-inflammatory; vasotrophic; anti-anginal; anti-lythmic;  
XX CNS; central nervous system; respiratory; anti-diarrhoeal; anti-diabetic;  
XX vitruide; hepatotropic; antibacterial; anti-nausea; anti-emetic;  
XX dermatological; antitumor; antihypertensive; gene therapy; GPCR modulator; human;  
XX gene; 88.  
XX  
XX Homo sapiens.

XX MO2004040000-A2.  
 XX 13-MAY-2004.  
 XX 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 XX 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 XX Galenaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,  
 XX Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX MPI; 2004-390329/36.  
 XX P-PSDB; ADO29416.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 XX compounds that modulates diagnosing and treating disease condition  
 XX associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 XX pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 1029; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
 XX (GPCRs) and nucleic acids encoding them. The invention also relates to  
 XX sequences at least 90% identical to the GPCR proteins and nucleic acids  
 XX of the invention; methods of treating, preventing or diagnosing diseases  
 XX associated with GPCRs of the invention; methods of screening for  
 XX compounds useful in the treatment of GPCR-related diseases; a transgenic  
 XX mouse comprising a GPCR gene of the invention; a mouse comprising a  
 XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 XX from the transgenic mice; kits comprising several mice, each of which has  
 XX a mutation in a different GPCR gene of the invention; and kits comprising  
 XX probes which hybridize to GPCR polynucleotides of the invention. The  
 XX invention further discloses variants of the GPCR polypeptides and vectors  
 XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 XX be used in the diagnosis, treatment or prevention of a wide variety of  
 XX diseases including neurological disorders (e.g., Alzheimer's disease,  
 XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 XX disorders of the adrenal gland; disorders of the colon or intestine  
 XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 XX myocardial infarction); muscular disorders; blood disorders (e.g.,  
 XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 XX diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 XX nucleic acid of the invention. Note: The full sequence data for this  
 XX patent did not form part of the printed specification; those sequences  
 XX not shown were obtained in electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2064 BP; 384 A; 701 C; 541 G; 438 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 12; Length 2064;

XX Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTCGAGTTCTCGATGAGAT 21

XX 186 TTTCGAGTTCTCGATGAGAT 166

XX RESULT 30  
 XX AAD39154/C  
 XX ID AAD39154 standard; cDNA; 2082 BP.  
 XX AC AAD39154;

XX 04-OCT-2002 (first entry)  
 XX Human AP4AR cDNA.  
 XX Human; diadenosine tetraphosphate receptor; G-protein coupled receptor;  
 XX cardiovascular disorder; central nervous system disorder; hypertension;  
 XX cardioprotective activity; genitourinary system disorder; vasodilation;  
 XX myocardial ischaemia; immunological disorder; prophylaxis; AP4AR; AP4A;  
 XX GPR56; vaccine; therapy; gene; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 1..2082  
 XX FT /\*tag= a  
 XX FT /product= "Human AP4AR protein"

XX WO200234781-A1.

XX 02-MAY-2002.

XX 16-OCT-2001; 2001WO-EP011953.

XX 20-OCT-2000; 2000EP-00122836.

XX (SOLV ) SOLVAY PHARM GMBH.

XX Berger C, Tulp MM, Van RJ;

XX MPI; 2002-479707/51.

XX P-PSDB; AAE24077.

XX Identifying ligands or modulators of a G-protein coupled diadenosine  
 XX Tetraphosphate (AP4A) receptor for e.g. treating hypertension, by  
 XX measuring the binding of AP4A to the receptor in the presence or absence  
 XX of a candidate substance.

XX Claim 1; Page 11; 65pp; English.

XX The invention relates to a method for identifying/determining ligands for  
 XX human diadenosine Tetraphosphate (AP4A) receptor (AP4AR) which is a G-  
 XX protein coupled receptor (GPR56). The method is used for identifying  
 XX ligands, agonists or antagonists of the AP4AR polypeptide. The novel  
 XX substance is useful for the treatment, alleviation and/or prophylaxis of  
 XX an AP4AR-related dysfunction, disorder or disease particularly those  
 XX associated with the cardiovascular system e.g. hypertension or  
 XX vasodilation, regulation of haemostasis, myocardial ischaemia, ischaemic  
 XX preconditioning or cardioprotective activity, central nervous system),  
 XX glucose and insulin metabolism, immunological disorders or disorders of  
 XX genitourinary system. AP4AR polypeptide or gene is also useful as  
 XX vaccines for inducing immunological responses in a mammal. The present  
 XX sequence is human AP4AR cDNA

XX Sequence 2082 BP; 386 A; 707 C; 546 G; 443 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 6; Length 2082;

XX Best Local Similarity 100.0%; Pred. No. 5.8; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTCGAGTTCTCGATGAGAT 21

XX 186 TTTCGAGTTCTCGATGAGAT 166

XX RESULT 31  
 XX ABX16439/C  
 XX ID ABX16439 standard; DNA; 2231 BP.  
 XX AC ABX16439;  
 XX 15-APR-2003 (first entry)  
 XX

DE DNA encoding human SNORF10 receptor.  
 XX  
 XX SNORF10; receptor; human; inflammation; arthritis; autoimmune disease;  
 KW transplant rejection; graft vs. host disease; infection; septicemia;  
 KW AIDS; pain; psychotic disorder; neurological disorder; anxiety;  
 KW depression; locomotor problem; respiratory disorder; asthma; obesity;  
 KW eating disorder; body weight disorder; bulimia; diabetes; anorexia;  
 KW nausea; hypertension; hypotension; vascular disorder; cancer; ulcer;  
 KW cardiovascular disorder; ischemia; stroke; urinary retention;  
 KW sexual disorder; reproductive disorder; circadian rhythm disorder;  
 KW renal disorder; bone disease; osteoporosis; benign prostatic hypertrophy;  
 KW gastrointestinal disorder; nasal congestion; allergy;  
 KW Parkinson's disease; Alzheimer's disease; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX 5'UTR 1..72 /\*tag= a  
 XX CDS 73..2136 /\*tag= b  
 XX /\*product= "SNORF10 receptor"  
 XX 3'UTR 2137..2231 /\*tag= c  
 XX  
 XX US2002151704-A1.  
 XX 17-OCT-2002.  
 XX 22-OCT-2001; 2001US-00011370.  
 XX 05-APR-1999; 99US-00286085.  
 XX  
 XX (BORO/) BOROMSKY B E.  
 XX (OCGOZ/) OCGOZALEK K L.  
 XX (KIAM/) KIAM H.  
 XX (PACH/) PACHIRANA M S.  
 XX (SMITH/) SMITH K E.  
 XX  
 XX Borowsky BE, Ogozalek KL, Kyaw H, Pachtirana MS, Smith KE;  
 XX MPI: 2003-198335/19.  
 XX P-PSDB; ABG74441.  
 XX  
 XX New recombinant nucleic acid comprising a nucleic acid encoding a  
 PT mammalian SNORF10 receptor, useful for screening antagonist to the  
 PT SNORF10 receptor or as probes to obtain homologous nucleic acids from  
 PT other species.  
 XX  
 XX Claim 2; Fig 1A-D; 19pp; English.  
 XX  
 XX The invention describes a recombinant nucleic acid comprising a nucleic  
 CC acid encoding a mammalian SNORF10 receptor, which hybridizes under  
 CC stringent conditions to a nucleic acid encoding a human SNORF10 receptor  
 CC and having a sequence identical to the sequence of the human SNORF10  
 CC receptor-encoding nucleic acid contained in plasmid pEX2-SNORF10-f. The  
 CC nucleic acid is useful for expressing receptors they encode in  
 CC transfected cells, for screening antagonists to the SNORF10 receptor or  
 CC as probes to obtain homologous nucleic acids from other species and to  
 CC detect the existence of nucleic acids having complementary sequences in  
 CC samples. The protein is useful for treating pathophysiological conditions  
 CC such as chronic and acute inflammation, arthritis, autoimmune disease,  
 CC transplant rejection, graft vs. host disease, bacterial, fungal,  
 CC protozoan and viral infections, septicemia, AIDS, pain, psychotic and  
 CC neurological disorders, anxiety, depression, schizophrenia, dementia,  
 CC mental retardation, memory loss, epilepsy, locomotor problems,  
 CC respiratory disorders, asthma, eating/body weight disorders, obesity,  
 CC bulimia, diabetes, anorexia, nausea, hypertension, hypotension, vascular  
 CC and cardiovascular disorders, ischemia, stroke, cancer, ulcers, urinary  
 CC retention, sexual/reproductive disorders, circadian rhythm disorders,  
 CC renal disorder, bone diseases, osteoporosis, benign prostatic  
 CC hypertrophy, gastrointestinal disorders, nasal congestion, allergies,

CC Parkinson's disease and Alzheimer's disease. This sequence encodes the  
 CC novel human SNORF10 receptor  
 XX  
 XX Sequence 2231 BP; 418 A; 759 C; 587 G; 467 T; 0 U; 0 Other;  
 SQ  
 Query Match 95.5%; Score 21; DB 8; Length 2231;  
 Best Local Similarity 100.0%; Pred. No. 5.8;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 DB 238 TTGGAGTTCTCGATGAGAT 238  
 RESULT 32  
 AAK51502/c  
 ID AAK51502 standard; cDNA; 2713 BP.  
 XX  
 XX AAK51502;  
 AC  
 XX 06-NOV-2001 (first entry)  
 DT  
 XX  
 DE Human polynucleotide SEQ ID NO 47.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157190-A2.  
 XX 09-AUG-2001.  
 XX 05-FEB-2001; 2001WO-US004098.  
 XX  
 XX 03-FEB-2000; 2000US-00496914.  
 XX 27-APR-2000; 2000US-00560875.  
 XX 20-JUN-2000; 2000US-00598075.  
 XX 19-JUL-2000; 2000US-00620325.  
 XX 01-SEP-2000; 2000US-00654936.  
 XX 15-SEP-2000; 2000US-00663561.  
 XX 20-OCT-2000; 2000US-00693325.  
 XX 30-NOV-2000; 2000US-00728422.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejntman T, Goodrich R;  
 XX  
 XX MPI: 2001-476283/51.  
 XX P-PSDB; AAM78369.  
 XX  
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.  
 PT  
 XX  
 XX Claim 1; Page 618-621; 622pp; English.  
 XX  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78333-AAM80302) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication

XX Sequence 2713 BP; 489 A; 930 C; 722 G; 571 T; 0 U; 1 Other;  
 XX  
 Query Match 95.5%; Score 21; DB 4; Length 2713;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
 DB 186 TTGGAGTTCTCGATGAGAT 166

RESULT 33  
 ADF70577/c  
 ID ADF70577 standard; DNA; 2796 BP.

XX ADF70577;  
 XX  
 XX 12-FEB-2004 (first entry)  
 XX  
 DE Orphan receptor ligand-related human protein gene SeqID200.

XX  
 KM ligand; orphan receptor protein; fusion protein; fluorescent protein;  
 KM cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;  
 KM GFPuv; Enhanced GFP; EGFP; human; gene; ds.

XX Homo sapiens.

XX WO2003071272-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003WO-JP001501.

XX 22-FEB-2002; 2002JP-00045728.

XX 23-JUL-2002; 2002JP-00213949.

XX 11-OCT-2002; 2002JP-00298237.

XX (TAKE ) TAKEEDA CHEM IND LTD.

XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;

XX WPI; 2003-697654/66.

XX P-PSDB; ADF70475.

XX Transformation of cells with a fusion protein of an orphan receptor  
 PT protein with a fluorescent protein useful for identification of ligands  
 PT to the orphan receptor.

XX Example 4; SEQ ID NO 200; 594pp; Japanese.

XX This invention relates to a novel method of identifying ligands to an  
 CC orphan receptor protein which comprises transforming cells with DNA  
 CC encoding a fusion protein of the orphan receptor with a fluorescent  
 CC protein, so that the fusion protein is expressed in the cells (or cell  
 CC membranes isolated from them) and contacting the cells with the potential  
 CC ligand to be tested. A suitable fluorescent protein (GFP), for example GFP-1,  
 CC the fusion protein is a green fluorescent protein (GFP), for example GFP-1,  
 CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
 CC identification of ligands binding to an orphan receptor protein.

XX Sequence 2796 BP; 617 A; 865 C; 697 G; 617 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 10; Length 2796;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
 DB 186 TTGGAGTTCTCGATGAGAT 166

RESULT 34

ADA14221/c  
 ID ADA14221 standard; cDNA; 2816 BP.

XX ADA14221;

XX 06-NOV-2003 (first entry)

XX Human GPR56-3 encoding cDNA SEQ ID NO:5.

XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
 KM gene therapy; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT 159..2240  
 FT /\*tag= a  
 FT /product= "GPR56-3"

XX WO2003068965-A1.

XX 21-AUG-2003.

XX 12-FEB-2003; 2003WO-AU000178.

XX 12-FEB-2002; 2002US-00073054.

XX (GTWO-) G2 THERAPIES LTD.

XX Herzog H, Sutherland RL, Mackay CR, Henshall S;

XX WPI; 2003-689676/65.

XX P-PSDB; ADA14222.

XX New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.

XX Example 1; Page 103-106; 129pp; English.

XX The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytosolic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence encodes the human GPCR,  
 CC designated GPR56-3, which is used in the exemplification of the present  
 CC invention.

XX Sequence 2816 BP; 517 A; 953 C; 758 G; 588 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 9; Length 2816;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
 DB 344 TTGGAGTTCTCGATGAGAT 324

RESULT 35  
 ADN39449/c  
 ID ADN39449 standard; cDNA; 2821 BP.

AC ADN39449;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:149.  
 XX  
 XX Human; differential expression; cancer; angiogenic disorder;  
 KM fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;  
 KM inflammatory disease; autoimmune disease;  
 KM retinal neovascularization syndrome; scarring; uterine fibroid;  
 KM detection; diagnosis; prognosis; drug screening; drug targeting;  
 KM wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
 KM vulnery; gene therapy; vaccine; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003042661-A2.  
 PN  
 XX  
 PD 22-MAY-2003.  
 XX  
 XX  
 PF 13-NOV-2002; 2002WO-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334933P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368099P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386146P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397755P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
 PI  
 XX  
 DR WPI: 2003-468649/44.  
 DR P-PSDB; ADN39450.  
 XX  
 XX  
 PT Determining the presence or absence of a pathological cell in a patient,  
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
 PT a nucleic acid in a biological sample.  
 XX  
 PS Claim 8; SEQ ID NO 149; 1385bp; English.  
 XX  
 XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiogenic or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.

SO Sequence 2821 BP; 516 A; 948 C; 765 G; 592 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 11; Length 2821;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCTCGATGAGAT 21  
 DB 348 TTCGAGTTCTCGATGAGAT 328  
 RESULT 36  
 AAK99413/C  
 ID AAK99413 standard; cDNA; 2822 BP.  
 XX  
 XX AAK99413;  
 AC  
 XX  
 DT 27-JUN-2002 (first entry)  
 XX  
 XX cDNA of human G protein coupled receptor GPR56.  
 DE  
 XX GPR56; anorectic; G protein-coupled receptor; orphan receptor; obesity;  
 KM appetite control test; transgenic animal; human; chromosome 16q13; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200183558-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 30-APR-2001; 2001WO-GB001865.  
 PR 03-MAY-2000; 2000US-0201422P.  
 PR  
 PA (ASTR) ASTRAZENECA AB.  
 PA (ASTR) ASTRAZENECA UK LTD.  
 XX  
 PI Brenand JC, Hart KA;  
 PI  
 XX  
 DR WPI: 2002-066520/09.  
 XX  
 XX  
 PT Use of G protein-coupled receptor, GPR56, to identify appetite control  
 PT agent by screening GPR56 agonists or antagonists and selecting active  
 PT agents by subjecting identified compounds to appetite control test  
 PT method.  
 XX  
 PS Claim 6; Page 14-15; 28pp; English.  
 XX  
 XX The invention relates to the use of a G protein-coupled receptor, GPR56,  
 CC for identifying appetite control agents comprising screening for agonists  
 CC and/or antagonists of GPR56 (an orphan receptor), using one or more  
 CC agonists and/or antagonists so identified as test compounds. In one or  
 CC more appetite control test procedures and selecting an active compound  
 CC for use as an appetite control agent. An agonist or antagonist of GPR56  
 CC identified by the method of the invention, is useful as an appetite  
 CC control agent for controlling appetite in an individual. The dominant  
 CC negative mutant of GPR56 is useful for evaluating the role of GPR56 in  
 CC the control of appetite. A transgenic non-human animal containing the  
 CC GPR56 gene is useful for evaluating the effects of test compounds in  
 CC appetite control and obesity. The agonists or antagonists of GPR56 are  
 CC useful as appetite control agents for controlling obesity. AON is also  
 CC useful as an appetite control agent. This polynucleotide sequence  
 CC represents the cDNA of the human G protein-coupled receptor, GPR56, of  
 CC the invention  
 XX  
 SO Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 6; Length 2822;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCTCGATGAGAT 21  
 |||||



Db 348 TTCGAGTCTCGATGAGAT 328

RESULT 37  
ABA05329/c  
ID ABA05329 standard; DNA; 2822 BP.

XX  
XX ABA05329;  
XX  
XX  
XX 27-FEB-2002 (first entry)  
XX  
XX Human GPR56 encoding DNA.  
XX  
XX Human; GPR22; anorectic; appetite control agent; GPR; gene;  
XX G protein-coupled receptor; orphan receptor; antisense gene therapy;  
XX mouse; GPR56; ds.

OS Homo sapiens.  
XX  
XX WO200183550-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 30-APR-2001; 2001WO-GB001874.  
XX  
XX 03-MAY-2000; 2000US-0201418P.  
XX  
XX (ASTR ) ASTRAZENECA AB.  
XX (ASTR ) ASTRAZENECA UK LTD.  
XX  
XX Brennan JC, Hart KA;  
XX  
XX WPI; 2002-066519/09.

PT Identifying appetite control agent for controlling obesity, comprises  
PT screening agonists or antagonists of G protein-coupled receptor, GPR22,  
PT and using them as test compounds in appetite control test procedures.

PS Claim 6; Page 18-19; 21pp; English.

XX The invention relates to identifying an anorectic appetite control agent,  
XX comprising screening for agonists and/or antagonists of G protein-coupled  
XX receptor GPR22 (an orphan receptor), using one or more agonists and/or  
XX antagonists so identified as test compounds in one or more appetite  
XX control procedures and selecting an active compound for use as an  
XX appetite control agent. An antisense oligonucleotide to the GPR22 gene is  
XX also useful for controlling obesity using antisense gene therapy. Note:  
XX The GPR22 encoding cDNA sequence (ABA05328) and encoded protein  
XX (AAM47903) are disclosed, however two DNA sequences described as human  
XX (ABA05328) and mouse (ABA05328) GPR56 are given in the sequence listing  
XX but are not otherwise referred to in the specification

XX  
XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
XX

Query Match 95.5%; Score 21; DB 6; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
DB 348 TTCGAGTCTCGATGAGAT 328

RESULT 38  
ABA242865/c  
ID ABA242865 standard; DNA; 2822 BP.

XX  
XX ABA242865;  
XX  
XX  
XX 04-MAR-2003 (first entry)  
XX  
XX Human G protein-coupled receptor TM7XN1/GPR56 DNA SEQ ID NO:517.  
XX

KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KM G protein-coupled receptor modulator; antibody; immune-related disease;  
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KM immunological-related cell proliferative disease; autoimmune disease;  
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KM ulcer; gene; ds.

OS Homo sapiens.  
XX  
XX WO200261087-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 19-DEC-2001; 2001WO-US050107.  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX Burmer GC, Roush CL, Brown JP;  
XX  
XX WPI; 2003-046718/04.  
XX  
XX P-PSDB; ABP82015.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.

XX  
XX Disclosure; Fig 1; 523pp; English.

PS The present invention describes antigenic peptides (1) comprising: (a)  
PS any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
PS acids; Also described: (1) an assay for the detection of a particular G  
PS protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
PS and (2) an isolated antibody having high specificity and high affinity or  
PS avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
PS gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
PS antibody against a particular GPCR, and in the production of specific  
PS antibodies. The peptides of corresponding GPCRs. The antigenic peptides for  
PS presence or absence of corresponding GPCRs. The antigenic peptides for  
PS GPCRs and antibodies are useful for diagnosing and designing drugs for  
PS treating immune-related diseases, growth-related diseases, cell  
PS regeneration-related disease, immunological-related cell proliferative  
PS diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
PS atherosclerosis, bacterial, fungal, protozoan or viral infections,  
PS osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
PS inflammation, allergies, Crohn's disease, diabetes, graft versus host  
PS disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
PS anxiety, depression, schizophrenia, dementia, mental retardation, memory  
PS loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
PS hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
PS any other disorder in which GPCRs are involved. The antibodies may be  
PS used in immunoassays and immunodiagnosis. ABA242523 to ABA242869 encode  
PS GPCR proteins given in ABP81675 to ABP82018, which are used in the  
PS exemplification of the present invention

XX  
XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
XX

Query Match 95.5%; Score 21; DB 8; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
DB 348 TTCGAGTCTCGATGAGAT 328

```
RESULT 39
ADA14217/c
ID ADA14217 standard; cDNA; 2822 BP.
XX
XX ADA14217;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human GPR56-1 encoding cDNA SEQ ID NO.1.
DE
XX
XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;
KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;
KM gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 163..2244
FT /tag= a
FT CDS /product= "GPR56-1"
XX
XX MO2003068965-A1.
PN
XX
XX 21-AUG-2003.
PD
XX
XX 12-FEB-2003; 2003WO-AU000178.
PF
XX
XX 12-FEB-2002; 2002US-00073054.
PR
XX
XX (GTWO-) G2 THERAPIES LTD.
PA
XX
XX Herzog H, Sutherland RL, Mackay CR, Henshall S;
PI
XX
XX WPI: 2003-689676/65.
DR P-PSDB; ADA14218.
XX
XX New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,
PT useful for preparing a composition for preventing, inhibiting or delaying
PT tumor growth.
PS
XX
XX Claim 1; Page 88-92; 129pp; English.
XX
XX The present invention describes a nucleic acid probe for detecting RNA
CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a
CC sample. Also described: (1) detecting a cancer cell in a subject; (2)
CC detecting ovarian cancer or its metastases in a subject; (3) determining
CC an effector memory T cell response in a subject; (4) determining whether
CC or not a subject has been re-infected with an infectious agent; (5)
CC determining the presence of effector memory T cells in a test sample; (6)
CC counting effector memory T cells in a subject; (7) detecting a cancer
CC cell in a subject; (8) reducing or preventing an inflammatory response in
CC a subject; (9) preventing, inhibiting or delaying tumour growth in a
CC subject; and (10) stimulating an immune response in a subject. GPR56 has
CC cytotaxic activity, and can be used in gene therapy. The nucleic acid
CC probe is useful for preparing a composition for preventing, inhibiting or
CC delaying tumour growth. The present sequence encodes the human GPCR,
CC designated GPR56-1, which is used in the exemplification of the present
CC invention.
XX
XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 9; Length 2822;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGAGGTTCTCGATGAGAT 21
DB 348 TTCGAGGTTCTCGATGAGAT 328
XX
XX RESULT 40
XX AAX25359/c
XX ID AAX25359 standard; cDNA; 2834 BP.
XX
```

```
XX
XX AAX25359;
AC
XX
XX 19-JUL-1999 (first entry)
DT
XX
XX Human G protein coupled receptor TSR32 cDNA.
DE
XX
XX TSR32; G protein coupled receptor; thyroid; human; Bardet Biedl syndrome;
KM ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 169..2250
FT /tag= a
FT CDS
XX
XX MO915551-A1.
PN
XX
XX 01-APR-1999.
PD
XX
XX 24-SEP-1998; 98WO-AU000805.
PF
XX
XX 24-SEP-1997; 97AU-0009386.
PR
XX
XX (GARV-) GARVAN INST MEDICAL RES.
PA
XX
XX Herzog H;
PI
XX
XX WPI: 1999-244386/20.
DR P-PSDB; AAY05730.
XX
XX New G-protein-coupled receptor designated TSR32.
PT
XX
XX Claim 5; 10-11; 23pp; English.
XX
XX This is the nucleotide sequence of an isolated polynucleotide, the coding
CC region of which is also claimed, encoding a new human G protein coupled
CC receptor, termed TSR32 (see AAY05730), which is a member of the secretin
CC receptor family. TSR32 is expressed in many tissue types, with highest
CC expression in the thyroid gland, suggesting that TSR32 has important
CC functions in metabolic regulation throughout the body via the thyroid
CC gland. TSR32 cDNA was isolated from a human heart cDNA library using a
CC 466 bp fragment that had itself identified using degenerate
CC oligonucleotides based on conserved regions of the human glucagon-like
CC peptide receptor family. The invention provides TSR32 polypeptides,
CC polynucleotides, a vector, host cells, an antibody and a non-human
CC transgenic animal, as well as a method for detecting agonists or
CC antagonists of TSR32, oligonucleotide or polynucleotide probes, an
CC antisense polynucleotide, and a method of producing TSR32 or its
CC polypeptides by culturing the host cells. The TSR32 protein, its agonists
CC and antagonists can be used to regulate thyroid functions in growth,
CC development and metabolic activity. The gene for TSR32 has been mapped to
CC chromosome 16q31, where Bardet Biedl syndrome, an autosomal recessive
CC disorder, has been linked
XX
XX Sequence 2834 BP; 520 A; 951 C; 767 G; 596 T; 0 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 2; Length 2834;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGAGGTTCTCGATGAGAT 21
DB 354 TTCGAGGTTCTCGATGAGAT 334
XX
XX RESULT 41
XX AAX35743/c
XX ID AAX35743 standard; cDNA; 3563 BP.
XX
XX AAX35743;
AC
XX
XX 09-JUL-1999 (first entry)
DT
```

XX DE cDNA encoding a protein identified by the signal sequence trap method.  
 XX XX  
 KW Signal sequence trap method; SST method; immunisation; inhibition;  
 KW infection; allergy; cancer; regulation; tissue formation; tissue repair;  
 KW actin activity; inhibin activity; chemokine activity;  
 KW cytokine activity; blood coagulation regulation; agonist; antagonist;  
 KW metabolic disorder; hormonal disorder; immune disorder;  
 KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;  
 KW ss.  
 XX OS Homo sapiens.  
 XX MO9918126-A1.  
 XX PN 15-APR-1999.  
 XX PD 06-OCT-1998; 98WO-JP004514.  
 XX PF 07-OCT-1997; 97JP-00274674.  
 XX PR (ONOV ) ONO PHARM CO LTD.  
 XX PA Fukushima D, Shibayama S, Tada H;  
 XX PI WPI; 1999-277254/23.  
 XX DR P-PSDB; AAY02382.  
 XX PT Polypeptides identified by the signal sequence trap method from a human  
 XX PT cDNA library.  
 XX PS Claim 5; Page 233-238; 281pp; Japanese.  
 XX CC AAX35694-X35747 represent cDNA sequences that encode novel polypeptides  
 CC (AAY02358-84) which are identified from a human placental cDNA library by  
 CC the signal sequence trap (SST) method. The polypeptides have a broad  
 CC range of physiological activity, including immunisation against and  
 CC inhibition of infections, allergies and cancer; regulation of tissue  
 CC formation and repair; actin/inhibin activity; chemokine/cytokine  
 CC activity; blood coagulation regulation; and receptor/ligand agonist or  
 CC antagonist activity. The polypeptides can be used for prevention and  
 CC treatment of disorders including infections by bacteria, yeasts and  
 CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;  
 CC immune disorders (including severe combined immunodeficiency (SCID) and  
 CC AIDS; thrombosis; cancer; and traumatic or surgical wounds  
 CC XX  
 SQ Sequence 3563 BP; 689 A; 1163 C; 934 G; 777 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 2; Length 3563;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 Db 228 TTGGAGTTCTCGATGAGAT 208  
 RESULT 42  
 ID AAA09348/C  
 XX AAA09348 standard; DNA; 3632 BP.  
 XX AC AAA09348;  
 XX XX 10-AUG-2000 (first entry)  
 XX DE G protein-coupled receptor protein 1 coding sequence.  
 XX XX  
 KW GPCR-1; G protein-coupled receptor protein; antipsoriatic; antineumatic;  
 KW epidermis-specific seven transmembrane receptor; HB6; immunosuppressive;  
 KW antiaesthetic; antineumatic; antiatherosclerotic; antichryoid; cyostatic;  
 KW hepatotropic; dermatological; anti-inflammatory; antihypertensive;  
 KW haemostatic; virucide; hepatotropic; osteopathic; antiparasitic;  
 KW immunostimulant; ss.

XX OS Homo sapiens.  
 XX XX  
 KW Key Location/Qualifiers  
 KW CDS 96..2177  
 KW FT /tag= a  
 KW FT  
 KW XX WO200020590-A2.  
 KW PN 13-APR-2000.  
 KW PD 06-OCT-1999; 99WO-US023317.  
 KW PF 06-OCT-1998; 98US-00167219.  
 KW PR 06-OCT-1998; 98US-0172211P.  
 KW PR 11-MAY-1999; 99US-0133585P.  
 KW XX  
 KW PA (INCY-) INCYTE PHARM INC.  
 KW XX Tang YT, Yue H, Lal P, Bandman O, Au-Young J, Reddy R;  
 KW PI Corley NC, Guegler KU, Gorgone GA, Baughn MR, Azimzal Y;  
 KW XX WPI; 2000-338934/28.  
 KW DR P-PSDB; AAY92362.  
 KW XX  
 KW PT Novel human G-protein coupled receptor proteins used in the diagnosis,  
 KW PT treatment and prevention of nervous system disorders,  
 KW PT autoimmune/inflammatory disorders, and cell proliferative disorders such  
 KW PT as cancer.  
 KW XX  
 KW PS Claim 9; Page 75; 84pp; English.  
 KW CC This sequence encodes human G-protein coupled receptor protein (GPCR) 1,  
 CC which has similarity with human epidermis-specific seven transmembrane  
 CC receptor HB6. The GPCR polypeptides, polynucleotides, antibodies,  
 CC antagonists and agonists may be administered to human patients for the  
 CC diagnosis, treatment and prevention of nervous system disorders (e.g.  
 CC epilepsy, stroke, neoplasms, Alzheimer's disease), autoimmune or  
 CC inflammatory disorders, complications of cancer, hemodialysis and  
 CC extracorporeal circulation, and cell proliferative disorders. They are  
 CC also used to treat or prevent disorders associated with decreased or  
 CC increased expression or activity of GPCR  
 CC XX  
 SQ Sequence 3632 BP; 700 A; 1187 C; 963 G; 782 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 3; Length 3632;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 Db 281 TTGGAGTTCTCGATGAGAT 261  
 RESULT 43  
 ID AAF28360/C  
 XX AAF28360 standard; CDNA; 3686 BP.  
 XX AC AAF28360;  
 XX XX 02-APR-2001 (first entry)  
 XX DE Human seven transmembrane receptor protein cDNA.  
 XX XX  
 KW Human; BBSR; Bardet-Biedl Syndrome Region; seven transmembrane receptor;  
 KW antidiabetic; anorectic; ophthalmological; antiinflammatory; noctropic;  
 KW cardiac; nephrotropic; gene therapy; chromosome 16;  
 KW retinal degeneration; hypogonadism; polydactyly; brachydactyly;  
 KW obesity; mental retardation; renal disorder; diabetes;  
 KW cardiovascular disorder; ss.  
 KW XX  
 XX OS Homo sapiens.

PN WO200100825-A2.  
XX  
PD 04-JAN-2001.  
XX  
XX 22-JUN-2000; 2000WO-US017375.  
XX  
PR 30-JUN-1999; 99US-0141753P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
PI Duhi D, Gorman SW;  
XX  
XX WPI; 2001-123009/13.  
DR P-PSDB; AAB61166.  
XX  
XX New human chromosome 15 and 16 Bardet-Biedl Syndrome Region polypeptide  
PT and polynucleotide for diagnosis and treatment of obesity, retinal  
PT degeneration, mental retardation, nervous system, heart and kidney  
PT disorders.  
XX  
XX Claim 2; Fig 5; 51pp; English.  
XX  
XX The present sequence is one of five novel Bardet-Biedl Syndrome Region  
CC (BBSR) polynucleotides that map to human chromosome 15 or 16. BBSR  
CC polynucleotides, polypeptides and anti-BBSR antibodies are useful for  
CC treating a BBSR protein-modulated disorder in a subject. An antibody that  
CC specifically binds to a BBSR protein is useful for diagnosing a BBSR  
CC protein-modulated disorder. BBSR protein-modulated disorders include  
CC Bardet-Biedl syndrome, retinal degeneration including retinitis  
CC pigmentosa, hypogonadism, polydactyly, brachydactyly, obesity, mental  
CC retardation, renal abnormalities, diabetes and cardiovascular  
CC abnormalities. BBSR polypeptides are also useful for screening  
CC combinatorial libraries to identify agonist or antagonists. Antibodies  
CC against BBSR polypeptides are useful for affinity chromatography, for  
CC distinguishing BBSR polypeptides and for inhibiting or modulating an  
CC activity or biological effect or a disorder associated with the BBSR  
CC proteins  
XX  
SQ Sequence 3686 BP; 737 A; 1192 C; 952 G; 803 T; 0 U; 2 Other;  
Query Match 95.5%; Score 21; DB 4; Length 3686;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGAGTCTCGATGAGAT 21  
DB 318 TTCCGAGTCTCGATGAGAT 298  
RESULT 44  
ADL26765/c  
ID ADL26765 standard; cDNA; 3702 BP.  
XX  
AC ADL26765;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human GPR56 encoding cDNA SEQ ID NO:19.  
XX  
XX ovarian cancer; ovarian cancer-associated transcript; cytostatic;  
KW gene therapy; human; GPR56; chromosome 16; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 159..2240  
FT /tag= a  
FT /product= "GPR56"  
XX  
XX WO2004022778-A1.  
XX  
XX 18-MAR-2004.  
XX

PF 05-SEP-2003; 2003WO-AU001166.  
XX  
XX 05-SEP-2002; 2002AU-00951346.  
PR  
XX  
XX (GARV-) GARVAN INST MEDICAL RES.  
XX  
XX Sutherland R, Henshall S, O'Brien P;  
XX  
XX WPI; 2004-315574/29.  
DR P-PSDB; ADL26766.  
XX  
XX Use of genes and proteins for diagnosing ovarian cancer and/or a  
PT likelihood for survival or recurrence of the disease.  
PT  
XX  
XX Claim 2; SEQ ID NO 19; 447pp; English.  
XX  
XX The present invention describes a method for the use of genes and  
CC proteins for diagnosing ovarian cancer and/or a likelihood for survival  
CC or recurrence of the disease, where the expression of genes and proteins  
CC is up-regulated and down-regulated or associated with the occurrence or  
CC recurrence of a specific cancer sub-type. Also described: (1) detecting  
CC an ovarian cancer-associated transcript in a biological sample; (2)  
CC diagnosing an ovarian cancer in a human or animal subject being tested;  
CC (3) detecting an ovarian cancer-associated polypeptide in a biological  
CC sample; (4) monitoring the efficacy of a therapeutic treatment of ovarian  
CC cancer; (5) determining the likelihood of survival of a subject suffering  
CC from an ovarian cancer; and (6) an assay device for use in the diagnosis  
CC or prognosis of ovarian cancer comprising polynucleotides or antibodies  
CC immobilised to a solid phase, where each of the polynucleotides consists  
CC of a gene given in the specification and each of the antibodies binds to  
CC a polypeptide also given in the specification and identifying a  
CC candidate compound for the treatment of ovarian cancer. An ovarian cancer  
CC -associated sequence has cytostatic activity, and can be used in gene  
CC therapy. An ovarian cancer-associated polynucleotide, vector, polypeptide  
CC or antibody can be used for the diagnosis or prognosis of ovarian cancer  
CC or for the preparation of a medicament for the treatment of ovarian  
CC cancer. The ovarian cancer that is diagnosed is an epithelial ovarian  
CC cancer selected from serous ovarian cancer, non-invasive ovarian cancer,  
CC mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrial  
CC ovarian cancer, clear cell ovarian cancer, papillary serous ovarian  
CC cancer, Brenner cell or undifferentiated adenocarcinoma. The present  
CC sequence encodes human GPR56, which is located on chromosome 16 and is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 3702 BP; 713 A; 1206 C; 973 G; 810 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 12; Length 3702;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGAGTCTCGATGAGAT 21  
DB 344 TTCCGAGTCTCGATGAGAT 324  
RESULT 45  
ADN95755/c  
ID ADN95755 standard; DNA; 3710 BP.  
XX  
AC ADN95755;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human BEC/LBC-related gene sequence SeqID679.  
XX  
XX growth; differentiation; blood endothelial cell; BEC;  
KW lymphatic endothelial cell; LBC; hereditary lymphedema; VEGFR-3;  
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;  
KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;  
KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;  
KW human.  
XX  
XX Homo sapiens.  
OS

```

XX  MO2003080640-A1.
XX
XX  02-OCT-2003.
XX
XX  07-MAR-2003; 2003WO-US006900.
XX
XX  07-MAR-2002; 2002US-0363019P.
XX
XX  (LUDW-) LUDWIG INST CANCER RES.
XX  (LICN ) LICENTIA LTD.
XX
XX  Alltalo K, Mäkinen T, Petrova T, Saharinen P, Saharinen J;
XX
XX  WPI; 2003-876899/81.
XX  P-PSDB; ADN95754.
XX
XX  Example 1; SEQ ID NO 679; 176pp; English.
XX
XX  This invention relates to a method of differentially modulating the
XX  growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX  endothelial cells (LEC) comprises contacting endothelial cells with a
XX  composition comprising an agent that differentially modulates blood or
XX  lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX  identifying a human subject with lymphoedema and with a mutation in at
XX  least one allele of a gene encoding a LEC protein, where the mutation
XX  correlates with lymphoedema in human subjects, and with the proviso that
XX  the LEC protein is not VEGFR-3; and administering to the subject a
XX  composition comprising a lymphatic growth agent selected from VEGF-C or
XX  VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX  the development of compounds with an antiangiogenic, cytostatic,
XX  vasotropic or antiinflammatory activity or for gene therapy. The method
XX  is useful in modulating the growth or differentiation of blood
XX  endothelial cells or lymphatic endothelial cells, in treating hereditary
XX  lymphoedema, in screening for an endothelial cell disorder or
XX  predisposition to the disorder or in monitoring the efficacy or toxicity
XX  of a drug on endothelial cells. The agent is useful in manufacturing a
XX  medicament for the differential modulation of blood vessel endothelial
XX  cell or lymphatic vessel endothelial cell growth or differentiation. The
XX  lymphatic growth agent may also be used in manufacturing a medicament for
XX  the treatment of hereditary lymphoedema resulting from a mutation in a
XX  LEC gene or of other diseases involving the lymphatic vessels, such as
XX  various inflammatory diseases and cancer metastasis via the lymphatic
XX  system. The present sequence is that of a human LEC/BEC differentially
XX  expressed gene which is related to the method of the invention. Note: This
XX  sequence does not appear in the specification but was obtained by the
XX  index using the source data given in table 14 of the specification.
XX
XX  Sequence 3710 BP; 714 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;
SQ
XX
XX  Query Match          95.5%; Score 21; DB 11; Length 3710;
XX  Best Local Similarity 100.0%; Pred. No. 6;
XX  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 TTCCGAGTTCGATGAGAT 21
XX  |||||||||||||||||||
XX  353 TTCCGAGTTCGATGAGAT 333
XX
XX  RESULT 46
XX  AAA49250/C
XX  ID AAA49250 standard; CDNA; 3711 BP.
XX
XX  AAA49250;
XX
XX  03-OCT-2000 (first entry)
XX
XX  Human seven transmembrane domain receptor zsig56 cDNA.
XX
XX  Human; zsig56; seven transmembrane domain receptor; hypotensive;
XX  antihypertensive; antiinflammatory; ion homeostasis; cardiac;
XX  neurotransmitter; neuroprotective; antiparkinsonian; cerebroprotective;
XX  neurotrophic; neuroleptic; tranquiliser; antianthratic; reproductive;
XX

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XX  signal transduction activator; bone disease; hypertension; renal failure;
XX  heart failure; hyperthyroidism; hyperparathyroidism; carcinoma;
XX  sarcoidosis; pancreatitis; stress; high blood pressure;
XX  immune depression; periodontal disease; neurodegenerative disease;
XX  multiple sclerosis; Alzheimer's disease; Parkinson's disease;
XX  schizophrenia; manic depression; stroke; rheumatoid arthritis;
XX  male fertility; spermatogenesis stimulation; pregnancy regulation;
XX  prostate cancer; ss.
XX
XX  Homo sapiens.
XX
XX  Key          Location/Qualifiers
XX  CDS           190..2271
XX              /*tag= a
XX              /product= "zsig56"
XX              /tag= b
XX              /tag= c
XX
XX  mat_peptide  265..2268
XX
XX  WO200034473-A2.
XX
XX  15-JUN-2000.
XX
XX  02-DEC-1999; 99WO-US028492.
XX
XX  10-DEC-1998; 98US-00208691.
XX
XX  (ZYMO ) ZYMOGENETICS INC.
XX
XX  Shepard PO, Elsworth Jr;
XX
XX  WPI; 2000-442164/38.
XX  P-PSDB; AAB01246.
XX
XX  Novel G-protein coupled receptor zsig56 useful for treating hypertension,
XX  hyper and hypothyroidism, inflammation, gout, carcinoma, pancreatitis,
XX  Alzheimer's disease and Parkinson's disease, renal and heart failure.
XX
XX  Claim 2; Page 104-109; 121pp; English.
XX
XX  The present sequence encodes a seven transmembrane domain receptor
XX  designated zsig56. The full length nucleotide sequence was obtained from
XX  a human retina library. zsig56 polypeptides, nucleic acid, agonists
XX  and/or antagonists may be used to treat a wide range of disorders
XX  including certain bone diseases, hypertension, renal failure, gout,
XX  congestive heart failure, hyperthyroidism, hyperparathyroidism, certain
XX  carcinomas, sarcoidosis and pancreatitis. They can be used to treat
XX  disorders associated with changes in ion or electrolyte homeostasis, and
XX  stress induced disorders such as high blood pressure, heart failure,
XX  immune depression and periodontal disease. They may be used to treat
XX  neurodegenerative diseases, including multiple sclerosis, Alzheimer's
XX  disease and Parkinson's disease, schizophrenia and manic depression, and
XX  to repair nerve tissue following damage due to strokes and brain and
XX  spinal injuries. Inflammatory disorders such as rheumatoid arthritis can
XX  also be treated. zsig56 is expressed in tissues associated with
XX  reproduction, i.e. the testis, prostate and placenta, and may be used to
XX  treat male fertility by stimulating spermatogenesis and to regulate
XX  gestation and birth. zsig56 may be useful as a marker or therapeutic
XX  agent in the treatment of prostate cancer
XX
XX  Sequence 3711 BP; 710 A; 1217 C; 971 G; 813 T; 0 U; 0 Other;
SQ
XX
XX  Query Match          95.5%; Score 21; DB 3; Length 3711;
XX  Best Local Similarity 100.0%; Pred. No. 6;
XX  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 TTCCGAGTTCGATGAGAT 21
XX  |||||||||||||||||||
XX  375 TTCCGAGTTCGATGAGAT 355
XX
XX  RESULT 47

```

AAD57428/c  
 ID AAD57428 standard; DNA; 3711 BP.  
 XX  
 AC AAD57428;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human TM7XN1 protein.  
 XX  
 KW Human; therapy; renal carcinoma; non-melanoma tumour; GPCR; astrocytoma; brain tumour; adenocarcinoma; G-protein coupled receptor; glioblastoma; tumour target protein; TM7XN1; cytotoxic; receptor; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 168..2249  
 FT /tag= a  
 FT /product= "Human TM7XN1 protein"  
 XX  
 PN WO2003057148-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 23-DEC-2002; 2002WO-US041419.  
 XX  
 PR 27-DEC-2001; 2001US-0343422P.  
 XX  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 PA (GONZ/) GONZALEZ-ZULUETA M.  
 XX  
 PI Gonzalez-Zulueta M, Mueller S, Foehr E, Chin D;  
 XX  
 DR WPI; 2003-598311/56.  
 DR P-PSDB; AAB38135.  
 XX  
 PT Treating brain tumor e.g., astrocytoma, or adenocarcinoma, non-melanoma  
 PT tumor and renal carcinoma by administering a compound that specifically  
 PT binds a TM7XN1 protein, and is conjugated to one or more cytotoxic  
 PT groups.  
 XX  
 PS Example 1; Page 66-70; 73pp; English.  
 XX  
 CC The invention relates to a method of treating brain tumour, renal  
 CC carcinoma, non-melanoma tumour and adenocarcinoma. The method involves  
 CC administering a compound that specifically binds a GPCR (G-protein  
 CC coupled receptor) tumour target protein, TM7XN1 where the compound is  
 CC conjugated to one or more cytotoxic groups. The method is useful for  
 CC treating brain tumour (e.g. astrocytoma preferably glioblastoma),  
 CC adenocarcinoma, non-melanoma tumour and renal carcinoma. The method is  
 CC useful for developing biologically active agents that modulate activity  
 CC of brain tumour target gene or gene product. The present sequence is  
 CC human TM7XN1 DNA  
 CC  
 SQ Sequence 3711 BP; 715 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;  
 XX  
 QY Query Match 95.5%; Score 21; DB 9; Length 3711;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 TTCGAGTCTCGATGAGAT 21  
 353 TTCGAGTCTCGATGAGAT 333  
 XX  
 RESULT 48  
 ID ADA14219/c  
 AC ADA14219 standard; cDNA; 3711 BP.  
 XX  
 AC ADA14219;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX

DE Human GPR56-2 encoding cDNA SEQ ID NO:3.  
 XX  
 XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KW GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
 XX gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 168..2249  
 FT /tag= a  
 FT /product= "GPR56-2"  
 XX  
 PN WO2003068965-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 12-FEB-2003; 2003WO-AU000178.  
 XX  
 PR 12-FEB-2002; 2002US-00073054.  
 XX  
 PA (GTWO-) G2 THERAPIES LTD.  
 XX  
 PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX  
 DR WPI; 2003-689676/65.  
 DR P-PSDB; ADA14220.  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Example 1; Page 95-99; 129pp; English.  
 XX  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytostatic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence encodes the human GPCR,  
 CC designated GPR56-2, which is used in the exemplification of the present  
 CC invention.  
 CC  
 SQ Sequence 3711 BP; 715 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;  
 XX  
 QY Query Match 95.5%; Score 21; DB 9; Length 3711;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 TTCGAGTCTCGATGAGAT 21  
 353 TTCGAGTCTCGATGAGAT 333  
 XX  
 RESULT 49  
 ID AAK94597/c  
 AC AAK94597 standard; cDNA; 3748 BP.  
 XX  
 AC AAK94597;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human full-length cDNA, SEQ ID NO: 3537.  
 DE Human, full length cDNA; cDNA synthesis; oligo-capping; ss.  
 XX

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XX OS Homo sapiens.
XX PN EP130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR WPI; 2001-524255/58.
XX DR P-PSDB; AAW93662.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Claim 8; SEQ ID NO 3537; 1380pp + Sequence Listing; English.
XX SQ The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO
XX SQ
SQ Sequence 3748 BP; 709 A; 1219 C; 1004 G; 816 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 3748;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
DB 430 TTCGAGTTCGATGAGAT 410

RESULT 50
ADL31504/c
ID ADL31504 standard; cDNA; 3748 BP.
XX AC ADL31504;
XX DT 20-MAY-2004 (first entry)
XX DE Full length human cDNA clone SeqID 3537.
XX DE human; medicine; signal transduction; glycoprotein; transcription;
XX DE oligo-capping method; ss; gene.
XX OS Homo sapiens.
XX PN EP1396543-A2.
XX PD 10-MAR-2004.
XX PF 07-JUL-2000; 2003EP-00025638.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.

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PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR WPI; 2004-204755/20.
XX DR P-PSDB; ADL31505.
XX PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX PT length human cDNAs.
XX PS Example 1; SEQ ID NO 3537; 1340pp; English.
XX SQ This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polynucleotide sequence is a
CC full length human cDNA clone of the invention.
XX SQ
SQ Sequence 3748 BP; 709 A; 1219 C; 1004 G; 816 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 12; Length 3748;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
DB 430 TTCGAGTTCGATGAGAT 410

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Search completed: February 2, 2005, 00:06:13  
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OM nucleic - nucleic search, using sw model

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Title: US-10-073-054-14  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues  
Total number of hits satisfying chosen parameters: 65645750

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	315	2	BE938539 RCO-TN008
2	21	95.5	383	4	BM151906 TCBAPE11
3	21	95.5	453	4	BM193168 TCBAPE10
4	21	95.5	464	2	AM844829 RC3-CN005
5	21	95.5	474	2	BE245815 TCBAPE11
6	21	95.5	475	2	BF841366 RC2-HT107
7	21	95.5	496	5	BE475238 DKEZP686N
8	21	95.5	512	2	BE244425 TCBAPE16
9	21	95.5	515	2	BE391006 601285614
10	21	95.5	520	2	BE244892 TCBAPE127
11	21	95.5	522	2	BE243851 TCBAPE16
12	21	95.5	523	7	CN337098 170004706
13	21	95.5	524	2	BE019655 BM27104.X
14	21	95.5	527	2	AM837046 QV1-LT003
15	21	95.5	531	2	BE246307 TCBAPE16
16	21	95.5	532	5	BE475095 DKEZP686J
17	21	95.5	535	5	BE475050 DKEZP686H
18	21	95.5	542	5	BE475102 DKEZP686J
19	21	95.5	559	6	CA390929 ca116c02.
20	21	95.5	568	2	BE206268 ba96e12.x
21	21	95.5	570	1	AL707342 DKEZP686C
22	21	95.5	573	1	AL598371 DKEZP686K
23	21	95.5	583	5	BE475118 DKEZP686K
24	21	95.5	601	5	BX506361 DKEZP686N

25	21	95.5	607	5	BX485768
26	21	95.5	613	4	BG819058 602781132
27	21	95.5	618	4	BG819937 602782040
28	21	95.5	636	4	B176699 603054091
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30	21	95.5	649	1	AL046540
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32	21	95.5	697	4	B1666902 603291647
33	21	95.5	728	1	AL133937 DKEZP761P
34	21	95.5	732	1	B1767127 603054191
35	21	95.5	741	4	B1464202 603203303
36	21	95.5	752	4	BG910316
37	21	95.5	755	7	CN337099 170005315
38	21	95.5	757	4	BG705518 602686543
39	21	95.5	761	4	BG536985 602650545
40	21	95.5	773	4	B1907794 603066045
41	21	95.5	774	7	CF995022 AGENCOURT
42	21	95.5	777	5	BO433220 AGENCOURT
43	21	95.5	785	4	B1553947 603193818
44	21	95.5	806	4	B1601981 60324377
45	21	95.5	811	7	CF995140 AGENCOURT
46	21	95.5	817	6	CD246163 AGENCOURT
47	21	95.5	827	6	CB987979 AGENCOURT
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52	21	95.5	872	4	B1559738 603252621
53	21	95.5	889	5	BUI56180 AGENCOURT
54	21	95.5	908	5	BO432053 AGENCOURT
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67	21	95.5	1355	5	BO068139 AGENCOURT
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70	19.4	88.2	212	1	AI559387 AGENCOURT
71	19.4	88.2	317	2	BM193164 AGENCOURT
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73	18.8	85.5	218	9	CC661759 AGENCOURT
74	18.8	85.5	639	6	CB212094 AGENCOURT
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76	18.8	85.5	843	9	CG722513 AGENCOURT
77	18.8	85.5	881	9	CG254830 AGENCOURT
78	18.8	85.5	915	9	CG279152 AGENCOURT
79	18.8	85.5	979	9	CG259010 AGENCOURT
80	18.8	85.5	980	9	CG272523 AGENCOURT
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84	17.8	80.9	492	7	CF428016 AGENCOURT
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94	17.8	80.9	598	7	CO250299 AGENCOURT
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96	17.8	80.9	648	5	BX260861 AGENCOURT
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C 98	17.8	80.9	714	5	BP123251	BP123251	C 171	17.4	79.1	578	4	BG558905	BG558905
C 99	17.8	80.9	794	8	CC095404	CC095404	C 172	17.4	79.1	579	6	BG052669	BG052669
C 100	17.8	80.9	829	5	B036444	B036444	C 173	17.4	79.1	579	6	CA290804	CA290804
C 101	17.8	80.9	1003	5	BG527452	BG527452	C 174	17.4	79.1	583	4	BG948499	BG948499
C 102	17.4	79.1	167	2	BE356782	BE356782	C 175	17.4	79.1	584	7	CF571003	CF571003
C 103	17.4	79.1	172	6	CF027049	CF027049	C 176	17.4	79.1	585	2	BE358537	BE358537
C 104	17.4	79.1	190	8	BH622540	BH622540	C 177	17.4	79.1	585	4	BG356916	BG356916
C 105	17.4	79.1	204	6	CD990202	CD990202	C 178	17.4	79.1	586	5	BH897311	BH897311
C 106	17.4	79.1	217	8	BH622541	BH622541	C 179	17.4	79.1	586	6	CA129305	CA129305
C 107	17.4	79.1	318	2	AM498440	AM498440	C 180	17.4	79.1	587	6	CA222383	CA222383
C 108	17.4	79.1	329	2	D24342	D24342	C 181	17.4	79.1	587	6	CA109706	CA109706
C 109	17.4	79.1	353	4	B1128497	B1128497	C 182	17.4	79.1	587	6	CD207844	CD207844
C 110	17.4	79.1	356	2	BE362320	BE362320	C 183	17.4	79.1	589	4	BG051489	BG051489
C 111	17.4	79.1	384	1	A1964668	A1964668	C 184	17.4	79.1	589	6	CF049177	CF049177
C 112	17.4	79.1	386	2	BE351347	BE351347	C 185	17.4	79.1	589	6	CF049177	CF049177
C 113	17.4	79.1	406	1	AU197463	AU197463	C 186	17.4	79.1	589	7	CF628107	CF628107
C 114	17.4	79.1	426	4	BM328306	BM328306	C 187	17.4	79.1	589	7	CA257303	CA257303
C 115	17.4	79.1	426	4	AU161271	AU161271	C 188	17.4	79.1	590	6	CA293890	CA293890
C 116	17.4	79.1	430	1	AU091881	AU091881	C 189	17.4	79.1	591	6	CA220430	CA220430
C 117	17.4	79.1	440	7	BN10974	BN10974	C 190	17.4	79.1	591	6	CF049424	CF049424
C 118	17.4	79.1	440	7	CN800125	CN800125	C 191	17.4	79.1	591	6	BG559755	BG559755
C 119	17.4	79.1	441	6	CA180114	CA180114	C 192	17.4	79.1	592	4	BI808915	BI808915
C 120	17.4	79.1	444	4	BG836623	BG836623	C 193	17.4	79.1	594	4	CF071528	CF071528
C 121	17.4	79.1	452	6	CB628001	CB628001	C 194	17.4	79.1	594	6	BG559173	BG559173
C 122	17.4	79.1	454	2	BG048768	BG048768	C 195	17.4	79.1	595	5	BH896445	BH896445
C 123	17.4	79.1	467	2	BE050691	BE050691	C 196	17.4	79.1	595	5	BH896445	BH896445
C 124	17.4	79.1	483	6	CB834009	CB834009	C 197	17.4	79.1	598	4	CA276285	CA276285
C 125	17.4	79.1	485	4	CN517285	CN517285	C 198	17.4	79.1	600	6	CF060583	CF060583
C 126	17.4	79.1	495	4	BM358401	BM358401	C 199	17.4	79.1	600	6	CD231447	CD231447
C 127	17.4	79.1	500	6	CD988388	CD988388	C 200	17.4	79.1	605	4	BI074513	BI074513
C 128	17.4	79.1	507	4	BG357246	BG357246	C 201	17.4	79.1	605	4	CA109312	CA109312
C 129	17.4	79.1	508	6	CF308610	CF308610	C 202	17.4	79.1	606	4	BI099125	BI099125
C 130	17.4	79.1	509	6	CA210427	CA210427	C 203	17.4	79.1	606	6	CD231536	CD231536
C 131	17.4	79.1	511	4	BG103729	BG103729	C 204	17.4	79.1	608	6	CF051685	CF051685
C 132	17.4	79.1	512	6	CD989560	CD989560	C 205	17.4	79.1	608	7	CF485750	CF485750
C 133	17.4	79.1	512	6	CN146628	CN146628	C 206	17.4	79.1	608	7	CF571893	CF571893
C 134	17.4	79.1	513	6	CF027874	CF027874	C 207	17.4	79.1	608	7	CK318613	CK318613
C 135	17.4	79.1	515	6	CF236213	CF236213	C 208	17.4	79.1	610	1	A1649725	A1649725
C 136	17.4	79.1	516	6	CA233439	CA233439	C 209	17.4	79.1	610	6	CA070219	CA070219
C 137	17.4	79.1	517	4	BM419356	BM419356	C 210	17.4	79.1	614	4	BG356011	BG356011
C 138	17.4	79.1	519	6	CF304578	CF304578	C 211	17.4	79.1	615	6	CF071240	CF071240
C 139	17.4	79.1	521	6	CA126064	CA126064	C 212	17.4	79.1	615	6	BO410810	BO410810
C 140	17.4	79.1	528	2	BF481422	BF481422	C 213	17.4	79.1	619	4	BG605793	BG605793
C 141	17.4	79.1	530	6	CA202032	CA202032	C 214	17.4	79.1	619	5	BQ908654	BQ908654
C 142	17.4	79.1	532	6	CD991116	CD991116	C 215	17.4	79.1	619	7	CF427320	CF427320
C 143	17.4	79.1	538	6	CA255525	CA255525	C 216	17.4	79.1	620	6	BI139707	BI139707
C 144	17.4	79.1	540	2	BF421485	BF421485	C 217	17.4	79.1	620	6	CD221175	CD221175
C 145	17.4	79.1	540	7	CF433598	CF433598	C 218	17.4	79.1	621	6	CA255149	CA255149
C 146	17.4	79.1	541	6	CA203847	CA203847	C 219	17.4	79.1	621	6	A1691608	A1691608
C 147	17.4	79.1	545	4	BM419784	BM419784	C 220	17.4	79.1	622	6	CA245018	CA245018
C 148	17.4	79.1	545	6	CD986973	CD986973	C 221	17.4	79.1	622	6	BQ415422	BQ415422
C 149	17.4	79.1	546	6	BI129602	BI129602	C 222	17.4	79.1	623	6	CA149488	CA149488
C 150	17.4	79.1	546	6	CA242165	CA242165	C 223	17.4	79.1	623	6	CA154493	CA154493
C 151	17.4	79.1	546	6	CB290335	CB290335	C 224	17.4	79.1	623	6	CA928118	CA928118
C 152	17.4	79.1	547	6	CB087227	CB087227	C 225	17.4	79.1	623	6	CB380752	CB380752
C 153	17.4	79.1	548	2	BE601271	BE601271	C 226	17.4	79.1	623	6	CD426025	CD426025
C 154	17.4	79.1	550	5	BH897938	BH897938	C 227	17.4	79.1	624	6	CA268056	CA268056
C 155	17.4	79.1	552	6	CA219236	CA219236	C 228	17.4	79.1	625	2	BE356958	BE356958
C 156	17.4	79.1	553	6	CA219236	CA219236	C 229	17.4	79.1	625	6	CA256938	CA256938
C 157	17.4	79.1	553	4	A1714779	A1714779	C 230	17.4	79.1	625	7	CF234995	CF234995
C 158	17.4	79.1	553	4	BG050443	BG050443	C 231	17.4	79.1	625	7	CD233603	CD233603
C 159	17.4	79.1	553	4	CK102830	CK102830	C 232	17.4	79.1	627	1	AU088714	AU088714
C 160	17.4	79.1	554	4	CB925437	CB925437	C 233	17.4	79.1	628	1	BG948188	BG948188
C 161	17.4	79.1	557	4	BG101772	BG101772	C 234	17.4	79.1	628	6	CA133458	CA133458
C 162	17.4	79.1	561	4	BG101926	BG101926	C 235	17.4	79.1	628	6	CA230844	CA230844
C 163	17.4	79.1	561	4	CF430437	CF430437	C 236	17.4	79.1	630	6	CA299019	CA299019
C 164	17.4	79.1	561	2	CF573099	CF573099	C 237	17.4	79.1	631	6	CA290017	CA290017
C 165	17.4	79.1	564	2	BR355936	BR355936	C 238	17.4	79.1	631	6	CA404840	CA404840
C 166	17.4	79.1	564	4	BI140705	BI140705	C 239	17.4	79.1	632	6	CF311353	CF311353
C 167	17.4	79.1	566	2	BF481645	BF481645	C 240	17.4	79.1	633	6	CA163814	CA163814
C 168	17.4	79.1	570	6	CD985959	CD985959	C 241	17.4	79.1	640	6	CA243835	CA243835
C 169	17.4	79.1	571	6	CF034039	CF034039	C 242	17.4	79.1	640	6	CA243835	CA243835
C 170	17.4	79.1	573	6	CD430285	CD430285	C 243	17.4	79.1	640	7	CF433467	CF433467
C 170	17.4	79.1	577	4	BG051490	BG051490							

  

BG558905	RH122_52-	BG052669	RH122_28-	CA290804	SCUTSD202	BG948499	IP1_10_D1	CF571003	MCS008E02	BE358537	DL1_31_C1	BG356916	OV2_11_P0	BH897311	X054H10_P	CA163305	SCUFLB101	CA222383	SCSGFL403	CA109706	SCSGH107	CD207844	H81_35_A1	BG051489	FMI_57_B0	CA133936	SCUFLT101	CF049177	QC132D11.	CF628107	zmrw84_0	CA257303	SCSGFL419	CA293890	SCSGFLV100	CA220430	SCGBFL401	CD426364	SA1_20_B1	CF049424	QC136C05.	BG559755	RH122_73-	BI808915	E006A12_O	CF071528	FBI_17_G0	BG559173	RH122_75	BM660513	952039B10	CA276285	SCBPSD200	CF060583	QC111C05.	BI074513	IP1_16_B0	BI074513	IP1_16_B0	CA109312	SCSGH107	BI099125	IP1_38_A0	CD231536	PS1_22_D0.	CF051685	QC129906.	CF485750	PCW1_33_H	CF571893	MCSA030B0	CK318613	X9P01C06	A1649725	496008P08	CA070219	SCSGAD100	BO356011	EM1_19_C0	CF071240	FBI_16_H0	BO410810	GA_Ed003	BG605793	RH122_81	BO908654	T012E03_O	CF427320	PH1_4_C05	BI139707	IP1_48_B0	CD221175	CC1_74_G	CA255149	SCBFL417	A1691608	SCSGFL408	CA245018	GA_Ed009	BO419488	SCDIR2102	CA154493	SCVPR2204	CA928118	MTU6TR_P1	CB380752	3529_1_24	CD426025	SA1_15_D1	CA268056	SCCGFL411	BE356958	DG1_30_C1	CA256938	SCSGFL419	CF234995	PH1_22_B0	CA299019	SCSGFLB04	CA290017	SCAGFLB01	CA404840	EL01N0524	CF311353	ABF_-06-I	CA163814	SCBURZ308	CA243835	SCOGFL407	CF433467	NTT1_27_H
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C 244	17.4	79.1	641	2	BE358719	DG1_31_C1	C 317	17.4	79.1	708	7	CN140135	
C 245	17.4	79.1	641	4	BG442965	EA001	C 318	17.4	79.1	710	2	CN126772	
C 246	17.4	79.1	645	4	BG836312	ZM06_01G0	C 319	17.4	79.1	711	2	BF277169	
C 247	17.4	79.1	647	6	CA205659	SCCCE400	C 320	17.4	79.1	712	6	CA150121	
C 248	17.4	79.1	649	6	CA991974	HC0168_G1	C 321	17.4	79.1	720	1	AU094668	
C 249	17.4	79.1	651	1	AU165522	AU165522	C 322	17.4	79.1	722	1	AU162473	
C 250	17.4	79.1	653	6	CF071910	FEL_19_H1	C 323	17.4	79.1	724	2	AM563714	
C 251	17.4	79.1	654	5	BQ406787	GA_EB009	C 324	17.4	79.1	724	6	CA089032	
C 252	17.4	79.1	654	6	CA293956	SCSG1V100	C 325	17.4	79.1	726	6	CF231072	
C 253	17.4	79.1	655	6	CA145749	CA145749	C 326	17.4	79.1	726	6	CA404513	
C 254	17.4	79.1	655	6	CA225776	SCGR2005	C 327	17.4	79.1	733	7	CN524403	
C 255	17.4	79.1	656	4	BG322988	EM1_13_E1	C 328	17.4	79.1	734	6	CA068235	
C 256	17.4	79.1	656	6	CA145667	SCSGRT206	C 329	17.4	79.1	734	7	CF427801	
C 257	17.4	79.1	658	2	CD224446	CCCI_34_D	C 330	17.4	79.1	742	6	CB939076	
C 258	17.4	79.1	658	6	AM563254	LG1_204_A	C 331	17.4	79.1	744	7	CN140112	
C 259	17.4	79.1	658	6	CD425245	SA1_11_H1	C 332	17.4	79.1	748	7	CN152600	
C 260	17.4	79.1	659	5	BQ415536	GA_EB010	C 333	17.4	79.1	749	7	CN153460	
C 261	17.4	79.1	659	6	CA111815	SCCCLB102	C 334	17.4	79.1	754	6	CB628216	
C 262	17.4	79.1	662	6	CD208968	HSL_45_D1	C 335	17.4	79.1	754	7	CN520405	
C 263	17.4	79.1	663	6	CD233615	GA_EB006	C 336	17.4	79.1	765	7	CN126317	
C 264	17.4	79.1	663	3	AY111481	zda_may8	C 337	17.4	79.1	766	6	CA095025	
C 265	17.4	79.1	664	3	CD424364	SA1_5_B12	C 338	17.4	79.1	767	6	CB653970	
C 266	17.4	79.1	664	6	BQ411419	GA_EB003	C 339	17.4	79.1	769	6	CB653963	
C 267	17.4	79.1	665	5	CN142628	WOONDI_11	C 340	17.4	79.1	770	6	CA157721	
C 268	17.4	79.1	665	7	CA254164	SCSRT308	C 341	17.4	79.1	772	6	CB647749	
C 269	17.4	79.1	666	6	CN550292	SCSRT305	C 342	17.4	79.1	773	6	CB672075	
C 270	17.4	79.1	666	7	CB643203	OSJNEB03M	C 343	17.4	79.1	774	7	CN139603	
C 271	17.4	79.1	667	6	CN139439	OXI_22_C1	C 344	17.4	79.1	777	7	CN523554	
C 272	17.4	79.1	667	5	BQ409914	GA_EB002	C 345	17.4	79.1	781	7	CN128947	
C 273	17.4	79.1	669	5	CA269684	SCSRT308	C 346	17.4	79.1	782	9	CD615677	
C 274	17.4	79.1	670	6	CA260221	SCSRT305	C 347	17.4	79.1	784	6	CD446776	
C 275	17.4	79.1	671	6	CA162668	SCSRT305	C 348	17.4	79.1	788	6	CA280858	
C 276	17.4	79.1	672	6	CD437829	ELI1N0505	C 349	17.4	79.1	790	8	CN126236	
C 277	17.4	79.1	672	5	BQ402517	GA_EB005	C 350	17.4	79.1	791	8	BZ642506	
C 278	17.4	79.1	673	5	CA222218	SCSRT404	C 351	17.4	79.1	791	7	CN520907	
C 279	17.4	79.1	673	6	CA184958	SCSRT309	C 352	17.4	79.1	793	6	CB630455	
C 280	17.4	79.1	675	6	CA176596	SCSRT105	C 353	17.4	79.1	797	6	CB630455	
C 281	17.4	79.1	677	6	CA291983	SCAFL801	C 354	17.4	79.1	801	6	CN524493	
C 282	17.4	79.1	678	6	CA199113	SCSRT101	C 355	17.4	79.1	801	6	CA254935	
C 283	17.4	79.1	680	4	BI075093	IPI_19_H0	C 356	17.4	79.1	808	8	BE055592	
C 284	17.4	79.1	680	6	CA163358	SCSRT231	C 357	17.4	79.1	811	6	CA208616	
C 285	17.4	79.1	680	6	CA224152	SCSRT231	C 358	17.4	79.1	814	6	BE040228	
C 286	17.4	79.1	680	6	CA295005	SCSRT101	C 359	17.4	79.1	815	6	CB634771	
C 287	17.4	79.1	682	6	CN141681	WOONDI_1	C 360	17.4	79.1	815	6	CB632011	
C 288	17.4	79.1	682	6	CA222865	SCBFL404	C 361	17.4	79.1	819	6	CB628215	
C 289	17.4	79.1	682	7	CA237790	SCJFL301	C 362	17.4	79.1	820	9	CG294308	
C 290	17.4	79.1	682	6	CN128868	RHOH1_32	C 363	17.4	79.1	826	6	CA143311	
C 291	17.4	79.1	682	2	AM563366	LG1_204_E	C 364	17.4	79.1	827	7	CK092696	
C 292	17.4	79.1	683	2	CA116814	SCAFLR113	C 365	17.4	79.1	829	6	CN151038	
C 293	17.4	79.1	684	6	CA222869	SCBFL404	C 366	17.4	79.1	832	7	CB617841	
C 294	17.4	79.1	685	6	CN142634	WOONDI_11	C 367	17.4	79.1	834	6	CB620692	
C 295	17.4	79.1	686	7	CA927913	MTU6TR_P1	C 368	17.4	79.1	836	6	CB624051	
C 296	17.4	79.1	687	6	CF228101	PtAXM0008	C 369	17.4	79.1	837	6	CB624051	
C 297	17.4	79.1	688	6	CA134556	SCJFRT106	C 370	17.4	79.1	839	7	CK114583	
C 298	17.4	79.1	689	6	CA297630	SCCCSD2C0	C 371	17.4	79.1	841	6	CB642660	
C 299	17.4	79.1	690	6	CB642464	OSJNEB02K	C 372	17.4	79.1	846	6	CB653969	
C 300	17.4	79.1	691	6	CA934847	MTU5TS_P2	C 373	17.4	79.1	848	6	CA176237	
C 301	17.4	79.1	691	6	CA253001	SCJFL4009	C 374	17.4	79.1	858	4	BG446573	
C 302	17.4	79.1	693	6	CF231993	PtAXM0000	C 375	17.4	79.1	868	5	CB625914	
C 303	17.4	79.1	696	5	BU102722	SCCCAD100	C 376	17.4	79.1	878	6	CK419368	
C 304	17.4	79.1	696	5	CA064829	SCCCAD100	C 377	17.4	79.1	888	5	BX928943	
C 305	17.4	79.1	696	6	CA095173	SCCCCL500	C 378	17.4	79.1	888	5	CD446750	
C 306	17.4	79.1	697	6	CA155848	SCBFLR2300	C 379	17.4	79.1	891	8	CC133287	
C 307	17.4	79.1	697	6	CB656501	OSJNEC100	C 380	17.4	79.1	912	6	CA280826	
C 308	17.4	79.1	700	6	CA293074	SCAGFL804	C 381	17.4	79.1	917	7	CK418399	
C 309	17.4	79.1	701	6	CA102519	SCBGRH106	C 382	17.4	79.1	919	6	CA214908	
C 310	17.4	79.1	701	6	CA275028	SCBBD103	C 383	17.4	79.1	937	7	CA213462	
C 311	17.4	79.1	705	6	CA265543	SCBZRT306	C 384	17.4	79.1	964	6	CA103854	
C 312	17.4	79.1	705	7	BN356418	EM1_22_C1	C 385	17.4	79.1	975	6	CA271021	
C 313	17.4	79.1	707	4	CB685793	OSJNEB161	C 386	17.4	79.1	984	2	BE03760	
C 314	17.4	79.1	708	6	CB938303	IPCGJX13_	C 387	17.4	79.1	994	9	CG275351	
C 315	17.4	79.1	708	6	CB938303	IPCGJX13_	C 388	17.4	79.1	1062	6	CA282971	
C 316	17.4	79.1	708	6	CB938303	IPCGJX13_	C 389	17.4	79.1				

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C 390 17.4 79.1 1155 6 CA276199 SCCSD109
C 391 17.2 78.2 196 2 BA344481
C 392 17.2 78.2 279 7 CN846540
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C 397 17.2 78.2 479 7 M88858
C 398 17.2 78.2 480 1 AJ472025
C 399 17.2 78.2 484 1 BB859348
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C 401 17.2 78.2 497 8 AL332446
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C 403 17.2 78.2 540 1 AJ472026
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C 411 17.2 78.2 673 7 CF402160
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C 421 17.2 78.2 806 5 CR005579
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C 447 16.8 76.4 328 7 RI8135
C 448 16.8 76.4 376 5 BQ170967
C 449 16.8 76.4 394 4 BJ275455
C 450 16.8 76.4 424 1 AJ688657
C 451 16.8 76.4 434 6 CB793653
C 452 16.8 76.4 443 1 AL368804
C 453 16.8 76.4 461 6 CB736909
C 454 16.8 76.4 500 6 BI801703
C 455 16.8 76.4 501 5 BQ660427
C 456 16.8 76.4 513 9 P578R
C 457 16.8 76.4 552 2 BR482891
C 458 16.8 76.4 564 4 BJ18532
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C 466 16.8 76.4 615 4 BJ311743
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C 468 16.8 76.4 629 4 BJ783744
C 469 16.8 76.4 644 4 BI960126
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C 472 16.8 76.4 667 6 CB547646
C 473 16.8 76.4 668 6 CD873314
C 474 16.8 76.4 708 9 CL583352
C 475 16.8 76.4 711 7 CN241475
C 476 16.8 76.4 718 4 BJ788439
C 477 16.8 76.4 724 6 CD450219
C 478 16.8 76.4 740 5 BX837617
C 479 16.8 76.4 741 9 CL759084
C 480 16.8 76.4 752 7 CO564159
C 481 16.8 76.4 773 8 AO329029
C 482 16.8 76.4 777 8 AO796301
C 483 16.8 76.4 797 5 BP119852
C 484 16.8 76.4 806 5 BP119782
C 485 16.8 76.4 832 6 CD656280
C 486 16.8 76.4 847 8 AO329512
C 487 16.8 76.4 916 9 B2764990
C 488 16.4 74.5 142 8 B2764990
C 489 16.4 74.5 149 5 BQ975098
C 490 16.4 74.5 161 6 CA733208
C 491 16.4 74.5 199 6 CD738057
C 492 16.4 74.5 261 4 BG906745
C 493 16.4 74.5 280 1 AJ769564
C 494 16.4 74.5 291 2 BA404053
C 495 16.4 74.5 300 2 BA401214
C 496 16.4 74.5 360 1 AJ769564
C 497 16.4 74.5 362 2 BE122502
C 498 16.4 74.5 373 2 BE587223
C 499 16.4 74.5 382 2 BE428692
C 500 16.4 74.5 386 2 BE509013

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## ALIGNMENTS

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RESULT 1
LOCUS BE338539 315 bp mRNA linear EST 02-OCT-2000
DEFINITION RCO-TN0080-160800-024-a02 TN0080 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE338539
VERSION BE338539.1 GI:10465968
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 315)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,
Brustein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

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TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

```

Email: aslimp@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=4&R=RC0-TN0080-160  
800-024-a02&t3=2000-08-16&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 27  
High quality sequence stop: 315.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1b="TN0080"

/note="Organ: testis normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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221 TTGGAGTTCTCGATGAGAT 241

## RESULT 2

BM151906/c 383 bp mRNA linear EST 30-NOV-2001  
LOCUS TCBAP1B136 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP136, mRNA  
sequence.

ACCESSION BM151906  
VERSION BM151906.1 GI:17175760  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 383)

AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R., Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.

TITLE Pediatric Leukemia cDNA Sequencing Project (2001)  
JOURNAL Unpublished (2001)

COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@ccc.org

Seq primer: M13 primer.  
Location/Qualifiers

## FEATURES

source

1..383  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP136"

/sex="male"  
/issue\_type="leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"

/note="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;  
leukemia Baylor-HGSC project=TCBA"  
/clone\_1b="Pediatric pre-B cell acute lymphoblastic  
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/notes="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;

## ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
310 TTGGAGTTCTCGATGAGAT 290

## RESULT 3

BM193168 453 bp mRNA linear EST 13-DEC-2001  
LOCUS TCBAP1B062 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1062, mRNA  
sequence.

ACCESSION BM193168  
VERSION BM193168.1 GI:17651403  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 453)

AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R., Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.

TITLE Pediatric Leukemia cDNA Sequencing Project (2001)  
JOURNAL Unpublished (2001)

COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@ccc.org

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP1062"

/sex="male"  
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/lab\_host="DH10B"

/note="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;  
leukemia Baylor-HGSC project=TCBA"  
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/clone\_1b="Pediatric pre-B cell acute lymphoblastic  
leukemia Baylor-HGSC project=TCBA"  
/notes="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;  
leukemia Baylor-HGSC project=TCBA"

## ORIGIN

normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T., Itoh M., Nagasaka S., Sasaki N., Okazaki Y., Muramatsu M., Schneider C., Hayashizaki Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

Query Match 95.5%; Score 21; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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Db 310 TTGGAGTTCTCGATGAGAT 290

RESULT 4  
AW844829/c 464 bp mRNA linear EST 18-MAY-2000  
LOCUS RC3-CN0056-010400-016-C04 CN0056 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW844829  
AW844829.1 GI:7938812

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 464)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M., R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunslein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE 10737800  
PUBMED 20202663

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2=RC3-CN0056-010400-016-C04&t3=2000-04-01&t4=1)

Seq primer: puc 18 forward  
High quality sequence start: 20  
High quality sequence stop: 464.

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/db\_xref="taxon:9606"  
/dev\_stage="Adult"

/clone\_lib="CN0056"  
/note="Organ: colon normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 20;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||

Db 390 TTGGAGTTCTCGATGAGAT 370

RESULT 5  
BE245815/c 474 bp mRNA linear EST 03-OCT-2001  
LOCUS TCBAPIE3171 Pediatric pre-B cell acute lymphoblastic leukemia

DEFINITION BE245815  
BE245815.1 GI:9097562

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 474)  
Wei, Y., Tsang, Y.T.M., Mei, G., Xu, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric leukemia cDNA Sequencing Project  
Unpublished (2000)

Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@tccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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Db 50 TTGGAGTTCTCGATGAGAT 30

RESULT 5  
BE245815/c 474 bp mRNA linear EST 03-OCT-2001  
LOCUS TCBAPIE3171 Pediatric pre-B cell acute lymphoblastic leukemia

DEFINITION BE245815  
BE245815.1 GI:9097562

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 474)  
Wei, Y., Tsang, Y.T.M., Mei, G., Xu, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric leukemia cDNA Sequencing Project  
Unpublished (2000)

Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@tccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.

Location/Qualifiers  
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/clone="TCBAP3171"

/sex="male"  
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/cell\_type="pre-B cell"

/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"

/clone\_lib="pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"

/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GAGGAGCTCGAGCGCGAGAGAG(T)VN 3'; V=A,C,G, N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGATCGCGCGCGCATTAATATAT(C) 3'] Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library was constructed by Wei Yu at RIKEN normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T., Itoh M., Nagasaka S., Sasaki N., Okazaki Y., Muramatsu M., Schneider C., Hayashizaki Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 474;  
Best Local Similarity 100.0%; Pred. No. 20;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||

Db 390 TTGGAGTTCTCGATGAGAT 370

RESULT 6  
BF841366/c

LOCUS BF841366 475 bp mRNA linear EST 13-JAN-2001  
DEFINITION RC2-HT1079-011200-014-d09 HT1079 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF841366  
VERSION BF841366.1 GI:12194291  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 475)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2&t=RC2-HT1079-011200-014-d09&c3=2000-12-01&t=1)  
Seq primer: puc 18 forward  
High quality sequence start: 18  
High quality sequence stop: 473.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HT1079"  
/note="Organ: head neck; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 475;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
DB 34 TTCCGAGTTCTCGATGAGAT 14

RESULT 7  
BX475238/c

LOCUS BX475238 496 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686N24175.t1 686 (synonym: hlc3) Homo sapiens cDNA clone  
ACCESSION BX475238  
VERSION BX475238.1 GI:31669432  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 496)  
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, W. and Wiemann, S.  
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
Unpublished (2003)  
JOURNAL COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine University, Duesseeldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No sequence available.  
This clone (DKFZp686N24175) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlc3)"  
/note="Vector: pTriblax2; Site\_1: SfiIA; Site\_2: SfiIB; cDNA-collection"

FEATURES  
source

ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 496;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
DB 485 TTCCGAGTTCTCGATGAGAT 465

RESULT 8  
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LOCUS BE244425 512 bp mRNA linear EST 03-OCT-2001  
DEFINITION TCBAP2E1627 Pediatric pre-B cell acute lymphoblastic leukemia  
ACCESSION BE244425  
VERSION BE244425.1 GI:9096166  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 512)  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Wei, Y., Tsang, Y.T.M., Mei, G., Xu, J.M., Ali-Osman, J.R., Wuzy, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric leukemia cDNA Sequencing Project  
Unpublished (2000)  
JOURNAL COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@tccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.  
Location/Qualifiers  
1..512  
/organism="Homo sapiens"



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/mol_type="mRNA"
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/dev_stage="pediatric 2 years"
/lab_host="DHOB"
/clone_lib="pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project-TCBA"
/note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'GAGAGACTCGAGCGCGCGCAGAG
3'; V=A,C,G; N=A,C,G,T) and then dg tailed. Second strand
was primed with a BamHI-dC primer
(5'AGAGAGCTCGGATCCGCGCGCGCGAGATTAATAT(C) 3'1.
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamI and SalI sites of
lambda PSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Garinini P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoaka S, Saekian I, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y. High efficiency selection of
full-length cDNA by improved biotinylated cap trapper..
DNA Res 4: 1 61-6, Feb 28, 1997)"

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**ORIGIN**

Query Match	95.5%	Score 21	DB 2	Length 512
Best Local Similarity	100.0%	Pred. No. 20		
Matches	21	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	1	TTGGAGTTTCGATGAGAT	21	
Db	274	TTGGAGTTTCGATGAGAT	254	

RESULT 9			
BE391006/c			
LOCUS	BE391006	515 bp	mRNA
DEFINITION	601285614p1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3607443 5', _	linear	EST 21-JUL-2000

ACCESSION	BE391006	GI:9336371
VERSION	BE391006.1	
KEYWORDS	EST.	human
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	

REFERENCE 1 (bases 1 to 515)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.

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FEATURES
source      location/Qualifiers
            1. .515
Plate: LTCM258  row: 1  column: 04
High quality sequence start: 9
High quality sequence stop: 506.

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/db xref=taxon:9606"
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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
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/note=Organ: uterus; Vector: pOT7; Site.1: XhoI; Site.2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-DNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies). "

	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
Qy	1	TTGGAGGTTCCGATGAGAT	21				
Db	476	TTGGAGGTTCCGATGAGAT	456				

	RESULT	10
BE244892/c		
LOCUS	BE244892	520 bp mRNA linear
DEFINITION	TCAPLIE2779 Pediatric pre-B cell acute lymphoblastic leukemia	EST_03-OCT-2001
		RNA

ORGANISM	Homo sapiens	Chordata; Vertebrata; Euteleostomi;
SOURCE	Homo sapiens (human)	
KEYWORDS	EST.	
VERSION	BE244892	
ACCESSION	BE244892.1	GI:9096722

REFERENCE	1 (bases 1 to 520)
AUTHORS	Wei, Y., Tang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman Jr., F. R., Muzny, D., Bouck, J., Gibbs, R. A. and Margolin, J. F.
TITLE	Pediatric Leukemia cDNA Sequencing Project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Dr. Judith F. Margolin

CONTACT: Dr. Utafan P. Matzoulin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Tel: 832-825-4038  
Fax: 832-825-4038  
Email: [clones@xccc.org](mailto:clones@xccc.org)  
Citation: Carninci, P. and Hayashibara, Y. High efficiency  
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M3 primer.

FEATURES	location/Qualifiers
source	1. .520

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/organism="Homo sapiens"
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/clone="TCBAp2779"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_1ib="pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project-TCBA"
/notes="Vector: lambda psb; site 1: BamHI; site 2: EcoRI;
first strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GAGAGCTCGAGCGCGCAGAGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGATCCGCGCGCCGCAATATATATAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda psb vector. Library was constructed by Wei Yu at RIKEN
normalization library.
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper."

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ORIGIN DNA Res 4: 1, 61-6, Feb 28, 1997"

Query Match 95.5%; Score 21; DB 2; Length 520;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
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DB 420 TTGGAGTTCGATGAGAT 400

RESULT 11  
BE243851/c 522 bp mRNA linear EST 03-OCT-2001  
LOCUS TCGAP1627 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC Project-TCBA Homo sapiens cDNA clone TCBAP1627, mRNA  
Sequence.

ACCESSION BE243851 GI:9095590  
VERSION BE243851  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 522)  
Wei, Y., Tang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R.,  
Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric Leukemia cDNA Sequencing Project  
Unpublished (2000)  
Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clone@ccccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency  
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M3 primer

FEATURES  
source  
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Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP1627"  
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/tissue\_type="Leukophoresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/clone\_1b="Pediatric pre-B cell acute lymphoblastic  
leukemia Baylor-HGSC Project-TCBA"  
/note="Vector: lambda psb; site 1: BamHI; site 2: EcoRI;  
first strand cDNA was primed with an anchored  
XhoI-oligo(dT) primer [5'-GAGAGCTCGAGCGCGCAGAGCAG(T)VN  
3'-V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
was primed with a BamHI-dC primer  
[5'-AGAGAGCTCGAGCGCGCGCGCAATTAATATAT(C) 3'].  
Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda psb vector. Library was constructed by Wei Yu at RIKEN  
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsuni T,  
Itoh M, Nagaoaka S, Sasaki, Okazaki Y, Muramatsu M,  
Schneider C, Hayashizaki Y. High efficiency selection of  
full-length cDNA by improved biotinylated cap trapper.  
DNA Res 4: 1, 61-6, Feb 28, 1997)"

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 522;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
|||||  
DB 273 TTGGAGTTCGATGAGAT 253

RESULT 12  
CN337098/c 523 bp mRNA linear EST 16-MAY-2004  
LOCUS 17000470616619 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
DEFINITION CN337098  
ACCESSION CN337098.1 GI:47337032  
VERSION EST.  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 523)  
Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M.S., Mandalam, R.,  
Lebkoweki, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6) 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 523 Std Error: 0.00.  
Location/Qualifiers

FEATURES  
source  
1..523  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_1b="GRN EB"  
/note="Oligo dT primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from h9 cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
|||||  
DB 393 TTGGAGTTCGATGAGAT 373

RESULT 13  
BE019655/c 524 bp mRNA linear EST 06-JUN-2000  
LOCUS db27h04.x1 NIH MGC 5 Homo sapiens cDNA clone IMAGE:2964151 3'  
DEFINITION similar to TR:095966 O95966 TM7XN1 PROTEIN PRECURSOR. ;, mRNA  
sequence.  
ACCESSION BE019655  
VERSION BE019655.1 GI:8279736  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 524)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: [imgc.llnl.gov/image/html/resources.shtml](http://imgc.llnl.gov/image/html/resources.shtml)

Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 405.

## FEATURES

## source

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1. 524
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2864151"
/tissue_type="carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NH MGC 5"
/note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCCGAGTTCTCGATGAGAT 21

182 TTCCGAGTTCTCGATGAGAT 162

## Db

RESULT 14  
 AM837046/c 527 bp mRNA linear EST 18-MAY-2000  
 LOCUS AM837046  
 DEFINITION QV1-LT0037-150200-069-e09 LT0037 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM837046  
 VERSION AM837046.1 GI:7931020  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,F., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=est2=QV1-LT0037-150200-069-e09&l3=2000-02-15&l4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 81.

## FEATURES

## source

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## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 527;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCCGAGTTCTCGATGAGAT 21

247 TTCCGAGTTCTCGATGAGAT 227

## Db

RESULT 15  
 BE246307/c 531 bp mRNA linear EST 03-OCT-2001  
 LOCUS BE246307  
 DEFINITION TCBAPE3B1627 pediatric pre-B cell acute lymphoblastic leukemia  
 BAYLOR-HGSC project=TCBA Homo sapiens cDNA clone TCBAPE1627, mRNA sequence.

ACCESSION BE246307  
 VERSION BE246307.1 GI:9098056  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,Y., Gibbs,R.A. and Margolin,J.F.  
 Pediatric Leukemia cDNA Sequencing Project  
 Unpublished (2000)  
 CONTACT: Dr. Judith F. Margolin  
 Texas Children's Cancer Center and Human Genome Sequencing Center  
 at Baylor College of Medicine  
 1102 Bates, MC3-3320 Houston, TX 77030, USA  
 Tel: 832-824-4536  
 Fax: 832-825-4038

TITLE  
 JOURNAL  
 COMMENT Email: clones@ccc.org  
 Citation: Carnucci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Seq primer: M13 primer.  
 Location/Qualifiers

## FEATURES

## source

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/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_1b="pediatric pre-B cell acute lymphoblastic leukemia BAYLOR-HGSC project=TCBA"
/note="Vector: lambda PSB, Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo (dT) primer 5'GGAGACTGACGGCCGCGAGAGAG(7)VN
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3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dc primer [5'AGAGAGCTCGATCCGCGCCGCAATTAATATAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 531;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
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Db 274 TTGGAGTTCTCGATGAGAT 254

RESULT 16  
BX475095/c 532 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686J10174.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZp686J10174.5', mRNA sequence.  
ACCESSION BX475095  
VERSION BX475095.1 GI:3169290  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobbo, G., Han, M., and Wiemann, S.  
TITLE (Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

FEATURES  
source  
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/clone="DKFZp686J10174"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_1lb="686 (synonym: hlcc3)"  
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cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 532;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 486 TTGGAGTTCTCGATGAGAT 466

RESULT 17  
BX479505/c 535 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686H07211.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZp686H07211.5', mRNA sequence.  
ACCESSION BX479505  
VERSION BX479505.1 GI:31915331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 535)  
Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobbo, G., Han, M., and Wiemann, S.  
TITLE (Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

FEATURES  
source  
1..535  
/organism="Homo sapiens"  
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cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 535;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCTCGATGAGAT 21  
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Db 432 TTGGAGTTCTCGATGAGAT 412

RESULT 18  
BX475102/c 542 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686J20174.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZp686J20174.5', mRNA sequence.  
ACCESSION BX475102  
VERSION BX475102.1 GI:3169297  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 542)  
Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobbo, G., Han, M., and Wiemann, S.  
TITLE (Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,  
 sequenced by GAP (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No at sequence available.  
 This clone (DKFZ66320174) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

## source

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 /lab\_host="DH10B"  
 /clone\_idb="686 (synonym: hicc3)"  
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 cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTGGAGTTCTCGATGGAGAT 21  
 |||||  
 500 TTGGAGTTCTCGATGGAGAT 480

## Db

RESULT 19  
 CA390929/c 559 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA390929  
 DEFINITION c116c02.y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c116c02  
 5', mRNA sequence.

ACCESSION CA390929  
 VERSION CA390929.1 GI:24722374  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Wistow, G., Bernstein, S.L., Wyatt, M.K., Paria, R.N., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Expressed sequence tag analysis of human RPE/choroid for the  
 NIHBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL MEDLINE  
 PUBMED 22103460  
 COMMENT 12107410  
 Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gstaeme@helix.nih.gov  
 Plate: 116 row: c column: 02  
 Seq primer: M13RPI reverse primer (ABI).

## FEATURES

## source

1..559  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="c116c02"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_idb="Human Retinal pigment epithelium/choroid cDNA"

(Un-normalized, unamplified): "cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the SuperScript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>. The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTGGAGTTCTCGATGGAGAT 21  
 |||||  
 435 TTGGAGTTCTCGATGGAGAT 415

## Db

RESULT 20  
 BE206268/c 568 bp mRNA linear EST 18-SEP-2000  
 LOCUS BE206268  
 DEFINITION ba96e12.x1 NIH MGC 5 Homo sapiens cDNA clone IMAGE:2925166 3'  
 similar to TR:059566 O95966 TM7XN1 PROTEIN PRECURSOR.; mRNA  
 sequence.

ACCESSION BE206268  
 VERSION BE206268.1 GI:8749666  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)  
 UNPUBLISHED (1999)  
 JOURNAL Contact: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 image.lnl.gov/image/html/lresources.shtml

Possible reversed clone: similarity on wrong strand  
 Seg primer: -40UP from Gibco  
 High quality sequence stop: 477.

## FEATURES

## source

1..568  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2925166"  
 /tissue\_type="carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_idb="NIH-MGC\_5"  
 /note="Organ: cervix; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACAGG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

	Query Match	95.5%;	Score 21;	DB 2;	Length 568;
	Best Local Similarity	100.0%;	Pred. No. 21;		
	Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1 TTGGAGTTCTCGATGAGAT 21       				
Db	298 TTCGAGTTCGATGAGAT 278				
RESULT 21					
AL707342/c	570 bp mRNA linear EST 04-SEP-2003				
DEFINITION	DKEZP686C1647.r1 686 (synonym: hicc3) Homo sapiens cDNA clone				
ACCESSION	DKEZP686C1647.5', mRNA sequence.				
VERSION	AL707342				
KEYWORDS	EST.				
SOURCE	AL707342.1 GI:19690697				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 570) Ottewaalder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weill,B. and Wiemann,S. EST (Ottewaalder,B., Obermaier,B., Mewes,H.W., Weill,B. and Wiemann,S.) Unpublished (2001)				
AUTHORS	Contact: MIPS				
TITLE	MIPS				
JOURNAL	Ingoltaedter Landstr.1, D-85764 Neubherg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; Sequenced by MediGenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. No si sequence available. This clone (DKEZP686C1647) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.				
FEATURES	Location/Qualifiers				
Source	1..570 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKEZP686C1647" /dev_stage="adult" /lab_host="DH10B" /clone_id="686 (synonym: hicc3)" /note="Vector: pTriplex2; Site_1: SfIRA; Site_2: SfIRB; cDNA-collection"				
ORIGIN					
Query Match	95.5%;	Score 21;	DB 1;	Length 570;	
Best Local Similarity	100.0%;	Pred. No. 21;			
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Oy	1 TTGGAGTTCTCGATGAGAT 21       				
Db	537 TTCGAGTTCGATGAGAT 517				
RESULT 22					
AL598371/c	573 bp mRNA linear EST 04-SEP-2003				
DEFINITION	DKEZP313A0720.r1 313 (synonym: hicc2) Homo sapiens cDNA clone				
ACCESSION	DKEZP313A0720.5', mRNA sequence.				
VERSION	AL598371				
KEYWORDS	EST.				
SOURCE	AL598371.1 GI:15161062				
ORGANISM	Homo sapiens (human)				
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 573)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS

MIPS
Inpolaedter Landetr.1, D-85764 Neuherberg, Germany
this is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olegen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFPZ313A0720) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers

FEATURES
source
1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFPZ313A0720"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="313 (synonym: hlcc2)"
/ncbi_vector="PTripEx2; Site_1: sfla; Site_2: sflb;
cdna-collection"

ORIGIN
Query Match 95.5%; Score 21; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TTGGAGTTCGATGGAGAT 21
|||||
513 TTGGAGTTCGATGGAGAT 493

RESULT 23
BX475118/c 583 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION
DKFPZ686K09174.F1 686 (synonym: hlcc3) Homo sapiens CDNA clone
DKFPZ686K09174.5', mRNA sequence.
BX475118
BX475118.1 GI:31669313
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS

MIPS
Inpolaedter Landetr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFPZ686K09174) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers

1..583
/organism="Homo sapiens"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 573)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS

MIPS
Inpolaedter Landetr.1, D-85764 Neuherberg, Germany
this is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olegen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFPZ313A0720) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers

FEATURES
source
1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFPZ313A0720"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="313 (synonym: hlcc2)"
/ncbi_vector="PTripEx2; Site_1: sfla; Site_2: sflb;
cdna-collection"

ORIGIN
Query Match 95.5%; Score 21; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TTGGAGTTCGATGGAGAT 21
|||||
513 TTGGAGTTCGATGGAGAT 493

RESULT 23
BX475118/c 583 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION
DKFPZ686K09174.F1 686 (synonym: hlcc3) Homo sapiens CDNA clone
DKFPZ686K09174.5', mRNA sequence.
BX475118
BX475118.1 GI:31669313
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS

MIPS
Inpolaedter Landetr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFPZ686K09174) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers

1..583
/organism="Homo sapiens"

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686K09174"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: sf1A; Site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 583;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGAGTCTCGATGAGAT 21  
Db 455 TTCCGAGTCTCGATGAGAT 435

## RESULT 24

LOCUS BX506361/c 601 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686N14249.r1 686 (synonym: hlcc3) Homo sapiens CDNA clone  
ACCESSION DKFZp686N14249.5', mRNA sequence.  
BX506361  
VERSION BX506361.1 GI:32040060  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 601)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Mewes, H.W., Well, B., Amd, C., Osanger, A., Fobo, G., Han, M. and  
Wiemann, S.  
EST (Ansoerge, W., Krieger, S., Regiert, T., Rittmuller, C., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp686N14249) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..601  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686N14249"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: sf1A; Site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 601;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGAGTCTCGATGAGAT 21  
Db 384 TTCCGAGTCTCGATGAGAT 364

## RESULT 25

BX485768/c 607 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686I13248.r1 686 (synonym: hlcc3) Homo sapiens CDNA clone  
DEFINITION DKFZp686I13248.5', mRNA sequence.  
BX485768  
ACCESSION BX485768  
VERSION BX485768.1 GI:31948835  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 607)  
Ostenwelder, B., Obermaier, B., Deutschenbauer, S., Mewes, H.W.,  
Well, B., Amd, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
EST (Ostenwelder, B., Obermaier, B., Deutschenbauer, S., Mewes, H.W.,  
et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence  
available.  
This clone (DKFZp686I13248) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..607  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686I13248"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: sf1A; Site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 607;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGAGTCTCGATGAGAT 21  
Db 400 TTCCGAGTCTCGATGAGAT 380

## RESULT 26

LOCUS BG819058/c 613 bp mRNA linear EST 22-MAY-2001  
DEFINITION BG819058.1 NCBI CGAP\_Brn67 Homo sapiens CDNA clone IMAGE:4932318  
5', mRNA sequence.  
BG819058  
ACCESSION BG819058  
VERSION BG819058.1 GI:14166645  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 613)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Query Match 95.5%; Score 21; DB 5; Length 613;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGAGTCTCGATGAGAT 21  
Db 400 TTCCGAGTCTCGATGAGAT 380



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM10857 row: 0 column: 07  
High quality sequence stop: 612.  
Location/Qualifiers

1. 613

## FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4932318"

/tissue\_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_1lb="NCI CGAP Brn67"

/note="Organ: Brain; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."

## ORIGIN

## Query Match

95.5%; Score 21; DB 4; Length 613;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21

DB 255 TTCCGAGTTCTCGATGAGAT 235

RESULT 27  
BG819937 618 bp mRNA linear EST 22-MAY-2001  
LOCUS 602782040F1 NCI CGAP Brn67 Homo sapiens CDNA clone IMAGE:4933089

DEFINITION 5', mRNA sequence.

ACCESSION BG819937 GI:14167524

VERSION BG819937.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 618)  
NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM10859 row: 0 column: 10  
High quality sequence stop: 616.

Location/Qualifiers

1. 618

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4933089"

/tissue\_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_1lb="NCI CGAP Brn67"

/note="Organ: Brain; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."

## ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21

DB 521 TTCCGAGTTCTCGATGAGAT 501

RESULT 28  
B1766999 636 bp mRNA linear EST 25-SEP-2001  
LOCUS 603054091F1 NIH\_MGC\_122 Homo sapiens CDNA clone IMAGE:5203583 5', mRNA sequence.

DEFINITION B1766999

ACCESSION B1766999.1 GI:15758577

VERSION EST.

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 636)  
NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM1510 row: e column: 24  
High quality sequence stop: 632.

Location/Qualifiers

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1lb="NIH\_MGC\_122"

/note="Organ: pooled lung and spleen; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; EcoRV (destroyed); RNA source anonymous pool of 24 week female lungs. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC library."

## ORIGIN

## Query Match

95.5%; Score 21; DB 4; Length 636;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21

DB 323 TTCCGAGTTCTCGATGAGAT 303

RESULT 29  
B1850146 643 bp mRNA linear EST 10-OCT-2001  
LOCUS B1850146

DEFINITION imagec10.2000/6158bdr81.y1 NCI CGAP Brn67 Homo sapiens CDNA clone IMAGE:4178114 5', mRNA sequence.

ACCESSION B1850146

VERSION B1850146.1 GI:16003633

KEYWORDS EST.

## ORIGIN

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 643)  
TITLE Kale, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and Prange, C.K.  
JOURNAL The I.M.A.G.E. Consortium quality control effort: clone resequencing for verification  
COMMENT Unpublished (2001)  
Contact: Prange CK  
The I.M.A.G.E. Consortium  
Lawrence Livermore National Laboratory  
Livermore, CA, USA  
Email: help@image.llnl.gov  
This read has been produced as part of the I.M.A.G.E. of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.  
plate: LLM9485 row: n column: 3  
Seq primer: ml3rpl  
High quality sequence stop: 643.  
Location/Qualifiers  
1..643  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4178114"  
/issue\_type="anaplastic oligodendroglioma with 1p/19q loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP Brn67"  
/note="Organ: Brain; Vector: PCMV-SPORE; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 95.5%; Score 21; DB 4; Length 643;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
522 TTGGAGTTCTCGATGAGAT 502

RESULT 30  
AL046540/c 649 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp34G178\_r1 434 (synonym: htes3) Homo sapiens cDNA clone  
DEFINITION DKFZp34G178 5', mRNA sequence.  
ACCESSION AL046540  
VERSION AL046540.1 GI:5434608  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 649)  
TITLE Othenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
JOURNAL EST (Othenwaelder, et al.)  
COMMENT Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de  
Sequenced by MedGenomix (Martinried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.  
This clone (DKFZp34G178) is available at the RZPD in Berlin.

FEATURES  
source  
1..649  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp34G178"  
/issue\_type="testis"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="434 (synonym: htes3)"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN  
Query Match 95.5%; Score 21; DB 4; Length 682;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
276 TTGGAGTTCTCGATGAGAT 256

RESULT 31  
BG718773/c 682 bp mRNA linear EST 08-MAY-2001  
LOCUS 602696925F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4628710 5',  
DEFINITION mRNA sequence.  
ACCESSION BG718773  
VERSION BG718773.1 GI:13997960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLM10747 row: b column: 07  
High quality sequence stop: 283.  
Location/Qualifiers  
1..682  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4628710"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_97"  
/note="Organ: testis; Vector: pBluescriptPR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (GCGGAG); Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
586 TTCCGAGTCTCGATGAGAT 566

RESULT 32  
B1666902/c 697 bp mRNA linear EST 12-SEP-2001

LOCUS 60329147F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:511282 5',  
mRNA sequence.

ACCESSION B1666902  
VERSION B1666902.1 GI:15581135  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 697)  
NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Place: L1AM11788 row: m column: 11  
High quality sequence stop: 674.

FEATURES  
Source Location/Qualifiers

1..697  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:511282"  
/issue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_96"  
/note="Organ: Brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcgag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTNN-3', size selected for average  
insert size 2.3 kb and normalized to R07 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC library."

# ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 697;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
367 TTCCGAGTCTCGATGAGAT 347

RESULT 33  
AL133937/c 728 bp mRNA linear EST 04-SEP-2003

LOCUS DKFZp761P0614\_F1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION DKFZp761P0614 5', mRNA sequence.  
ACCESSION AL133937  
VERSION AL133937.1 GI:6602124

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 728)  
Ansoorge, W., Wilkner, U., Mewes, W., Well, B. and Wiemann, S.  
EST (Ansoorge, W., Wilkner, U., Mewes, W., Well, B. and Wiemann, S.)  
Unpublished (1999)  
Contact: MIPS

MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.

No al sequence available.  
This clone (DKFZp761P0614) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
Source Location/Qualifiers

1..728  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp761P0614"  
/issue\_type="amygdala"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="761 (synonym: hamy2)"  
/note="Vector: pSPori1; Site\_1: NotI; Site\_2: SalI"

# ORIGIN

Query Match 95.5%; Score 21; DB 1; Length 728;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
393 TTCCGAGTCTCGATGAGAT 373

RESULT 34  
B1767127/c 732 bp mRNA linear EST 25-SEP-2001  
LOCUS 603054191F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5203607 5',  
mRNA sequence.

ACCESSION B1767127  
VERSION B1767127.1 GI:15758705  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 732)  
NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Place: L1AM1510 row: f column: 24  
High quality sequence stop: 724.  
Location/Qualifiers  
1..732

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203607"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleen. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

```

```

ORIGIN
Query Match      95.5%; Score 21; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      324 TTCCGAGTCTCGATGAGAT 304

```

```

RESULT 35
BI464202/c      741 bp      mRNA      linear      EST 21-AUG-2001
LOCUS      603203303F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269224 5',
DEFINITION      mRNA sequence.
ACCESSION      BI464202
VERSION      BI464202.1 GI:15254858
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      1 (bases 1 to 741)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Miklos Palkovics, M.D., Ph.D.
              CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
              Toshiyuki and Piero Carninci (RIKEN)
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11679 row: e column: 01
High quality sequence stop: 658.
Location/Qualifiers
1..741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269224"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTAA-3', size-selected for average
insert size 2.2 kb and normalized to ROR 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, In
preparation). Library constructed by M. Brownstein
(NH/NH/NHRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

```

## FEATURES

source

## ORIGIN

```

Query Match      95.5%; Score 21; DB 4; Length 741;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      515 TTCCGAGTCTCGATGAGAT 495

```

```

RESULT 36
BG910316/c      752 bp      mRNA      linear      EST 05-JUN-2001
LOCUS      602805910F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4938170
DEFINITION      5', mRNA sequence.
ACCESSION      BG910316
VERSION      BG910316.1 GI:114290792
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      1 (bases 1 to 752)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: David N. Louis, M.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10873 row: c column: 03
High quality sequence stop: 548.
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4938170"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

## FEATURES

source

## ORIGIN

```

Query Match      95.5%; Score 21; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      302 TTCCGAGTCTCGATGAGAT 282

```

```

RESULT 37
CN337099/c      755 bp      mRNA      linear      EST 16-MAY-2004
LOCUS      17000531597678 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION      CN337099
VERSION      CN337099.1 GI:47337033
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```


```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 755)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 755 Std Error: 0.00.  
Location/Qualifiers  
1..755  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_lib="GRN EB"  
/note="Oligo dt primed, full-length enriched cDNA library  
from embryoid body outgrowth derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 7; Length 755;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 516 TTCGAGTTCGATGAGAT 496

RESULT 38  
BG705518/c 757 bp mRNA linear EST 07-MAY-2001  
LOCUS 602686543F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4818826 5',  
mRNA sequence.  
ACCESSION BG705518  
VERSION BG705518.1 GI:13979935  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 757)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10721 row: f column: 11  
High quality sequence start: 67  
High quality sequence stop: 469.  
Location/Qualifiers  
1..757  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

FEATURES  
source

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 757;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 445 TTCGAGTTCGATGAGAT 425

RESULT 39  
BG536985/c 761 bp mRNA linear EST 03-APR-2001  
LOCUS 60265045F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4689874 5',  
mRNA sequence.  
ACCESSION BG536985  
VERSION BG536985.1 GI:13528531  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 761)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Clontech Laboratories, Inc.  
cDNA Library Preparation: Clontech Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM1506 row: i column: 11  
High quality sequence stop: 487.  
Location/Qualifiers  
1..761  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4689874"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:  
5'-ATTCTAGAGCCGAGCGCGCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

FEATURES  
source

Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 416 TTCGAGTTCGATGAGAT 396

RESULT 40  
BI907794 773 bp mRNA linear EST 16-OCT-2001  
LOCUS BI907794/c 603066045F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5215187 5',  
DEFINITION mRNA sequence.  
ACCESSION BI907794  
VERSION BI907794.1 GI:16170642  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incey Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LLAM1540 row: 1 column: 12  
High quality sequence stop: 773.

FEATURES  
source  
1. .773  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5215187"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6, Site 1: NotI, Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 4; Length 773;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 281 TTCGAGTTCGATGAGAT 261

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 773;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 281 TTCGAGTTCGATGAGAT 261

RESULT 41  
CF995022 774 bp mRNA linear EST 25-NOV-2003  
LOCUS CF995022  
DEFINITION AGENCOURT 15621840 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30528961 5', mRNA sequence.  
ACCESSION CF995022  
VERSION CF995022.1 GI:38511082  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Daniela S. Gerhard, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: NDAM615 row: m column: 02  
High quality sequence stop: 525.

FEATURES  
source  
1. .774  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30528961"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B Tona"  
/clone\_1lb="NIH\_MGC\_147"  
/note="Organ: Placenta; Vector: pBluescriptR; Site 1:  
all-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to R07 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 7; Length 774;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 465 TTCGAGTTCGATGAGAT 445

RESULT 42  
BQ433220/c 777 bp mRNA linear EST 24-MAY-2002  
LOCUS BQ433220  
DEFINITION AGENCOURT 7723723 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6050606  
5', mRNA sequence.  
ACCESSION BQ433220  
VERSION BQ433220.1 GI:21172296  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTB/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM13303 row: b column: 15

High quality sequence stop: 436.  
Location/Qualifiers

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1. 777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="6050606"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."
```

# ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 777;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
Db 465 TTCGAGGTTCTCGATGAGAT 445

RESULT 43  
BI553947 785 bp mRNA linear EST 05-SEP-2001  
LOCUS 603193818P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5264957 5',  
DEFINITION mRNA sequence.  
VERSION BI553947  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11668 row: c column: 06  
High quality sequence stop: 688.  
Location/Qualifiers

FEATURES  
source 1. 785

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5264957"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in
```

preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC library."

# ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 785;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
Db 534 TTCGAGGTTCTCGATGAGAT 514

RESULT 44  
BI601981 806 bp mRNA linear EST 07-SEP-2001  
LOCUS 603243977P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5286258 5',  
DEFINITION mRNA sequence.  
VERSION BI601981  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11723 row: j column: 19  
High quality sequence stop: 720.  
Location/Qualifiers

FEATURES  
source 1. 806

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5286258"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."
```

# ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 806;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCGAGGTTCTCGATGAGAT 21  
|||||  
Db 530 TTCGAGGTTCTCGATGAGAT 510.

RESULT 45



CF995140/c 811 bp mRNA linear EST 25-NOV-2003  
LOCUS AGENCOURT 15621962 NIH\_MGC\_147 Homo sapiens cDNA clone  
DEFINITION IMAGE:30527833 5', mRNA sequence.  
ACCESSION CF995140  
VERSION CF995140.1 GI:38511200  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 811)  
NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm.0A07 Bethesda, MD 20892  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: NDAM612 row: n column: 02  
High quality sequence stop: 640.  
Location/Qualifiers  
1. 811  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30527833"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B TONa"  
/clone\_1db="NIH\_MGC\_147"  
/note="Organ: placenta; Vector: pBluescriptR; Site: 1:  
all-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTTTTTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to R0T 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 7; Length 811;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGAGTCTCGATGGAGAT 21  
|||||  
Db 525 TTCCGAGTCTCGATGGAGAT 505  
|||||

RESULT 46  
CD246163 817 bp mRNA linear EST 22-MAY-2003  
LOCUS AGENCOURT 14127031 NIH\_MGC\_145 Homo sapiens cDNA clone  
DEFINITION IMAGE:6912793 5', mRNA sequence.  
ACCESSION CD246163  
VERSION CD246163.1 GI:31006627  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 817)  
NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: IRB101 row: d column: 12  
High quality sequence stop: 692.  
Location/Qualifiers  
1. 817  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6912793"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_1db="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.presv.dat  
a Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 817;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGAGTCTCGATGGAGAT 21  
|||||  
Db 202 TTCCGAGTCTCGATGGAGAT 182  
|||||

RESULT 47  
CB987979 827 bp mRNA linear EST 01-MAY-2003  
LOCUS AGENCOURT 13902574 NIH\_MGC\_147 Homo sapiens cDNA clone  
DEFINITION IMAGE:30340483 5', mRNA sequence.  
ACCESSION CB987979  
VERSION CB987979.1 GI:30282499  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 827)  
NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: NDAM370 row: g column: 20  
High quality sequence stop: 491.  
Location/Qualifiers  
1. 827  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30340483"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B TONa"  
/clone\_1lb="NIH\_MGC\_147"  
/note="Organ: Placenta; Vector: pBluescriptR, Site\_1: all-XhoI; Site\_2: BamHI; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to RQF 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Garnick, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH\_MGC library."

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 827;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
Db 525 TTGGAGTTCGATGAGAT 505

RESULT 48  
BP125765/c 835 bp mRNA linear EST 24-OCT-2000  
DEFINITION 601763157/1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4025774 5',  
mRNA sequence.  
ACCESSION BP125765  
VERSION BP125765.1 GI:10964805  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 835)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DC/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L16M855 row: b column: 15  
High quality sequence stop: 646.  
Location/Qualifiers

## FEATURES

1..835  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4025774"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_20"  
/note="Organ: skin; Vector: pOT57; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 835;  
Best Local Similarity 100.0%; Pred. No. 22;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGAGTTCGATGAGAT 21  
Db 470 TTGGAGTTCGATGAGAT 450

RESULT 49  
AL598478/c 840 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp313J2220 r1 313 (synonym: h1cc2) Homo sapiens cDNA clone  
LOCUS DKFZp313J2220 5', mRNA sequence.  
ACCESSION AL598478  
VERSION AL598478.1 GI:15161169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 840)  
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
TITLE EST (Duesterhoeft, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
This is from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Oigen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFZp313J2220) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..840  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp313J2220"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_1lb="313 (synonym: h1cc2)"  
/note="Vector: pTriplEx2; Site\_1: SfiI; Site\_2: SfiIb;  
cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 1; Length 840;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
Db 366 TTGGAGTTCGATGAGAT 346

RESULT 50  
BE893273/c 854 bp mRNA linear EST 20-OCT-2000  
LOCUS BE893273 601436985/1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:3921908 5',  
mRNA sequence.  
ACCESSION BE893273  
VERSION BE893273.1 GI:10354467  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 854)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DMP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: L1A8755 row: j column: 21  
 High quality sequence stop: 606.  
 Location/Qualifiers

## FEATURES

## source

1..854  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3921908"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH MGC 72"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
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 DB 403 TTCGAGTCTCGATGAGAT 383

Search completed: February 2, 2005, 01:27:37  
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Title: US-10-073-054-14

Perfect score: 22

Sequence: 1 ttctgagcttcctgagatgc 22

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

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# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	95.5	3819	4	US-10-140-002-405
C 2	16.4	74.5	441	4	US-09-252-991A-10248
C 3	16.4	74.5	1659	4	US-09-252-991A-10461
C 4	16.4	74.5	3267	4	US-09-252-991A-10707
C 5	16.2	73.6	519	4	US-09-252-991A-14488
C 6	16.2	73.6	1347	4	US-09-252-991A-15133
C 7	16.2	73.6	1465	4	US-09-252-991A-14625
C 8	16.2	73.6	1446	4	US-09-252-991A-15137
C 9	16.2	73.6	2001	4	US-09-689-012-1
C 10	16.2	73.6	2010	3	US-09-240-410-1
C 11	16.2	73.6	2154	4	US-09-252-991A-14624
C 12	16.2	73.6	2498	3	US-09-041-236-1
C 13	16.2	73.6	2622	4	US-09-771-467C-1
C 14	16.2	73.6	2698	4	US-09-252-991A-15001
C 15	15.8	71.8	550	4	US-09-668-751-133
C 16	15.8	71.8	744	4	US-09-270-767-14247
C 17	15.8	71.8	736	4	US-09-248-796A-414
C 18	15.8	71.8	1586	4	US-09-270-767-11307
C 19	15.8	71.8	1836	4	US-09-252-991A-6042
C 20	15.8	71.8	1911	4	US-09-252-991A-6258
C 21	15.6	70.9	251	4	US-09-016-434-320
C 22	15.6	70.9	393	4	US-09-328-352-3744
C 23	15.6	70.9	1095	4	US-09-602-787A-199
C 24	15.6	70.9	1371	4	US-09-492-709A-196
C 25	15.6	70.9	2637	4	US-09-799-875-3
C 26	15.6	70.9	3003	4	US-09-799-875-1
C 27	15.6	70.9	36470	4	US-08-311-731A-123

C 28	15.6	70.9	77536	4	US-09-410-551B-1	Sequence 1, Appl
C 29	15.6	70.9	77536	4	US-09-940-316B-1	Sequence 1, Appl
C 30	15.4	70.0	1686	4	US-09-799-451-327	Sequence 327, App
C 31	15.4	70.0	1984	4	US-09-377-466B-9	Sequence 9, Appl
C 32	15.4	70.0	1984	4	US-09-377-466B-11	Sequence 11, Appl
C 33	15.4	70.0	3039	4	US-09-377-466B-19	Sequence 19, Appl
C 34	15.4	70.0	3039	4	US-09-377-466B-21	Sequence 21, Appl
C 35	15.4	70.0	3450	4	US-09-377-466B-17	Sequence 17, Appl
C 36	15.4	70.0	3469	4	US-09-377-466B-23	Sequence 23, Appl
C 37	15.2	69.1	300	2	US-08-637-759B-8	Sequence 8, Appl
C 38	15.2	69.1	300	3	US-08-871-355A-8	Sequence 8, Appl
C 39	15.2	69.1	300	3	US-09-201-945-8	Sequence 8, Appl
C 40	15.2	69.1	413	4	US-09-621-976-15382	Sequence 15382, A
C 41	15.2	69.1	565	4	US-09-513-999C-12831	Sequence 12831, A
C 42	15.2	69.1	621	4	US-09-270-767-2463	Sequence 2463, Ap
C 43	15.2	69.1	621	4	US-09-270-767-17745	Sequence 17745, A
C 44	15.2	69.1	690	4	US-09-513-999C-1940	Sequence 1940, Ap
C 45	15.2	69.1	1047	4	US-09-602-787A-61	Sequence 61, Appl
C 46	15.2	69.1	1280	3	US-09-146-675-2	Sequence 2, Appl
C 47	15.2	69.1	1722	4	US-09-252-991A-9857	Sequence 9857, Ap
C 48	15.2	69.1	2547	4	US-09-548-938A-4	Sequence 4, Appl
C 49	15.2	69.1	3811	4	US-09-112-580-5	Sequence 5, Appl
C 50	15.2	69.1	5937	4	US-09-302-626B-59	Sequence 59, Appl
C 51	15.2	69.1	9706	4	US-09-843-250-5	Sequence 5, Appl
C 52	15.2	69.1	9841	4	US-09-843-250-10	Sequence 10, Appl
C 53	15.2	69.1	12808	4	US-09-843-250-10	Sequence 37, Appl
C 54	15.2	69.1	13417	2	US-08-637-759B-37	Sequence 37, Appl
C 55	15.2	69.1	13417	3	US-08-871-355A-37	Sequence 37, Appl
C 56	15.2	69.1	13417	3	US-09-201-945-37	Sequence 37, Appl
C 57	15.2	69.1	13863	4	US-09-814-915A-83	Sequence 83, Appl
C 58	15.2	69.1	14463	4	US-09-843-250-9	Sequence 9, Appl
C 59	15.2	69.1	174493	4	US-09-804-471A-3	Sequence 3, Appl
C 60	15.2	69.1	174493	4	US-10-238-709-3	Sequence 2, Appl
C 61	15.2	69.1	4403765	3	US-09-103-840A-2	Sequence 28774, A
C 62	15.2	69.1	4411529	3	US-09-513-999C-28774	Sequence 11, Appl
C 63	14.8	67.3	213	4	US-09-614-221A-71	Sequence 11, Appl
C 64	14.8	67.3	450	4	US-09-889-463A-11	Sequence 11, Appl
C 65	14.8	67.3	463	4	US-09-513-999C-1197	Sequence 1197, Ap
C 66	14.8	67.3	491	4	US-09-621-976-3788	Sequence 3788, Ap
C 67	14.8	67.3	972	4	US-09-270-767-10210	Sequence 10210, A
C 68	14.8	67.3	1773	4	US-09-248-796A-4887	Sequence 4887, Ap
C 69	14.8	67.3	1887	4	US-09-583-110-2646	Sequence 2646, Ap
C 70	14.8	67.3	1980	4	US-09-583-110-2647	Sequence 13, Appl
C 71	14.8	67.3	1980	4	US-09-889-463A-13	Sequence 38, Appl
C 72	14.8	67.3	1993	3	US-07-861-458C-38	Sequence 3, Appl
C 73	14.8	67.3	2237	3	US-08-456-647B-3	Sequence 3, Appl
C 74	14.8	67.3	2237	1	US-08-237-401A-3	Sequence 5215, Ap
C 75	14.8	67.3	2437	2	US-09-489-039A-5215	Sequence 5215, Ap
C 76	14.8	67.3	2463	4	US-09-489-039A-5330	Sequence 5330, Ap
C 77	14.8	67.3	2529	4	US-09-489-039A-5330	Sequence 351, App
C 78	14.8	67.3	5238	4	US-09-402-338-1	Sequence 1, Appl
C 79	14.8	67.3	5285	3	US-08-961-527B-52	Sequence 52, Appl
C 80	14.8	67.3	16593	3	US-09-453-702B-69	Sequence 69, Appl
C 81	14.8	67.3	26173	3	US-09-453-702B-116	Sequence 116, Appl
C 82	14.8	67.3	45175	4	US-09-457-855A-14	Sequence 117, App
C 83	14.8	67.3	118067	4	US-08-384-708A-117	Sequence 117, App
C 84	14.6	66.4	50	1	US-08-687-443-117	Sequence 117, App
C 85	14.6	66.4	50	3	US-08-444-423-117	Sequence 1812, Ap
C 86	14.6	66.4	272	4	US-09-313-234A-1812	Sequence 5253, Ap
C 87	14.6	66.4	295	4	US-09-313-234A-5253	Sequence 13015, A
C 88	14.6	66.4	360	4	US-09-513-999C-13115	Sequence 30781, A
C 89	14.6	66.4	370	4	US-09-270-767-30781	Sequence 7787, Ap
C 90	14.6	66.4	423	1	US-08-470-179-71	Sequence 23069, A
C 91	14.6	66.4	423	1	US-09-270-767-787	Sequence 145, App
C 92	14.6	66.4	506	4	US-09-270-767-23069	Sequence 4405, Ap
C 93	14.6	66.4	532	3	US-08-998-416-145	Sequence 447, App
C 94	14.6	66.4	532	3	US-09-252-991A-4405	Sequence 143, App
C 95	14.6	66.4	573	4	US-09-385-982-447	Sequence 129, App
C 96	14.6	66.4	584	3	US-08-998-416-143	Sequence 954, App
C 97	14.6	66.4	584	3	US-08-998-416-143	
C 98	14.6	66.4	638	3	US-08-998-416-143	
C 99	14.6	66.4	638	3	US-08-998-416-143	
C 100	14.6	66.4	641	4	US-09-620-312D-954	

101	14.6	66.4	666	4	US-09-252-991A-9833	Sequence 9833, Ap	C 174	14.6	66.4	3163	4	US-09-344-510B-6	Sequence 6, Appl
C 102	14.6	66.4	636	4	US-09-149-476-92	Sequence 92, Appl	C 175	14.6	66.4	3198	4	US-09-252-991A-15066	Sequence 15066, A
C 103	14.6	66.4	729	4	US-09-270-767-983	Sequence 783, Ap	C 176	14.6	66.4	3249	2	US-08-920-234-1	Sequence 1, Appl
C 104	14.6	66.4	729	4	US-09-270-767-23255	Sequence 22265, A	C 177	14.6	66.4	3435	4	US-09-252-991A-10017	Sequence 10017, A
C 105	14.6	66.4	834	4	US-09-710-279-1987	Sequence 1387, Ap	C 178	14.6	66.4	3435	4	US-09-344-510B-7	Sequence 7, Appl
C 106	14.6	66.4	834	4	US-09-248-796A-1248	Sequence 1248, Ap	C 179	14.6	66.4	3435	4	US-09-710-279-4114	Sequence 4114, Ap
C 107	14.6	66.4	846	3	US-09-105-537-942	Sequence 84, Appl	C 180	14.6	66.4	3518	4	US-09-976-594-279	Sequence 279, App
C 108	14.6	66.4	852	4	US-09-270-767-844	Sequence 844, App	C 181	14.6	66.4	3828	5	PCT-US93-03076-1	Sequence 1, Appl
C 109	14.6	66.4	852	4	US-09-270-767-16136	Sequence 16126, A	C 182	14.6	66.4	11219	3	US-07-642-734C-1	Sequence 1, Appl
C 110	14.6	66.4	858	4	US-09-489-039A-6335	Sequence 6335, Ap	C 183	14.6	66.4	11219	3	US-08-439-009A-1	Sequence 1, Appl
C 111	14.6	66.4	862	3	US-08-468-856B-4	Sequence 4, Appl	C 184	14.6	66.4	13613	3	US-09-105-537-3	Sequence 3, Appl
C 112	14.6	66.4	862	3	US-08-468-859A-4	Sequence 4, Appl	C 185	14.6	66.4	36778	3	US-09-105-537-5	Sequence 5, Appl
C 113	14.6	66.4	934	4	US-09-710-279-1531	Sequence 1531, Ap	C 186	14.6	66.4	38506	3	US-09-320-878-19	Sequence 19, Appl
C 114	14.6	66.4	966	4	US-09-252-991A-7439	Sequence 7439, Ap	C 187	14.6	66.4	38506	4	US-09-141-908-1	Sequence 1, Appl
C 115	14.6	66.4	972	4	US-09-252-991A-4609	Sequence 4609, Ap	C 188	14.6	66.4	45716	3	US-09-657-440-19	Sequence 19, Appl
C 116	14.6	66.4	987	4	US-09-252-991A-10022	Sequence 10022, A	C 189	14.6	66.4	45716	3	US-08-965-048-5	Sequence 5, Appl
C 117	14.6	66.4	993	4	US-09-252-991A-6760	Sequence 6760, Ap	C 190	14.6	66.4	45989	3	US-08-965-048-6	Sequence 6, Appl
C 118	14.6	66.4	1002	4	US-09-248-796A-1249	Sequence 1249, Ap	C 191	14.6	66.4	53615	4	US-09-214-808-1	Sequence 1, Appl
C 119	14.6	66.4	1035	4	US-09-252-991A-7201	Sequence 7201, Ap	C 192	14.6	66.4	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C 120	14.6	66.4	1061	4	US-09-270-767-14581	Sequence 14581, A	C 193	14.6	66.4	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C 121	14.6	66.4	1089	3	US-09-134-001C-1220	Sequence 1220, Ap	C 194	14.6	66.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 122	14.6	66.4	1112	3	US-09-434-288-9	Sequence 9, Appl	C 195	14.6	66.4	4403765	3	US-09-692-570-1	Sequence 1, Appl
C 123	14.6	66.4	1128	3	US-09-551-322-1	Sequence 1, Appl	C 196	14.6	66.4	4411529	3	US-09-103-840A-2	Sequence 1, Appl
C 124	14.6	66.4	1258	3	US-09-155-200-3	Sequence 10, Appl	C 197	14.6	66.4	4411529	3	US-09-103-840A-2	Sequence 1, Appl
C 125	14.6	66.4	1271	4	US-09-737-698B-10	Sequence 10, Appl	C 198	14.6	65.5	281	4	US-09-270-767-406	Sequence 406, App
C 126	14.6	66.4	1282	4	US-09-737-626A-10	Sequence 310, App	C 199	14.4	65.5	281	4	US-09-270-767-15688	Sequence 15688, A
C 127	14.6	66.4	1287	4	US-09-221-017B-310	Sequence 1287, A	C 200	14.4	65.5	460	2	US-08-487-727A-1	Sequence 1, Appl
C 128	14.6	66.4	1287	4	US-09-270-767-14276	Sequence 14276, A	C 201	14.4	65.5	514	4	US-09-270-767-7481	Sequence 7481, Ap
C 129	14.6	66.4	1350	4	US-09-149-476-248	Sequence 248, App	C 202	14.4	65.5	514	4	US-09-270-767-22763	Sequence 22763, A
C 130	14.6	66.4	1404	4	US-09-469-039A-5117	Sequence 5137, Ap	C 203	14.4	65.5	1830	3	US-08-969-683A-66	Sequence 66, Appl
C 131	14.6	66.4	1404	4	US-09-434-288-2	Sequence 2, Appl	C 204	14.4	65.5	2733	4	US-09-602-787A-577	Sequence 577, App
C 132	14.6	66.4	1419	4	US-09-252-991A-6853	Sequence 6853, Ap	C 205	14.4	65.5	2800	4	US-09-221-017B-668	Sequence 668, App
C 133	14.6	66.4	1463	4	US-09-398-522-113	Sequence 113, App	C 206	14.4	65.5	3812	1	US-08-188-582-19	Sequence 19, Appl
C 134	14.6	66.4	1463	4	US-09-252-991A-14444	Sequence 14444, A	C 207	14.4	65.5	3812	1	US-08-646-715-15	Sequence 15, Appl
C 135	14.6	66.4	1476	4	US-09-252-991A-15187	Sequence 15187, A	C 208	14.4	65.5	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 136	14.6	66.4	1521	2	US-09-004-502-2	Sequence 2, Appl	C 209	14.4	65.5	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 137	14.6	66.4	1521	3	US-09-360-125-2	Sequence 2, Appl	C 210	14.2	64.5	111	2	US-09-174-060-9	Sequence 9, Appl
C 138	14.6	66.4	1521	4	US-09-914-841A-14	Sequence 14, Appl	C 211	14.2	64.5	111	2	US-09-174-060-9	Sequence 9, Appl
C 139	14.6	66.4	1560	4	US-09-270-767-11208	Sequence 11208, A	C 212	14.2	64.5	111	3	US-08-338-382-8	Sequence 8, Appl
C 140	14.6	66.4	1713	4	US-09-252-991A-14948	Sequence 14948, A	C 213	14.2	64.5	111	3	US-08-338-382-8	Sequence 8, Appl
C 141	14.6	66.4	1797	4	US-09-252-991A-14444	Sequence 14444, A	C 214	14.2	64.5	111	4	US-09-345-264-8	Sequence 8, Appl
C 142	14.6	66.4	1800	4	US-09-737-698B-29	Sequence 29, Appl	C 215	14.2	64.5	111	4	US-09-345-264-9	Sequence 9, Appl
C 143	14.6	66.4	1800	4	US-09-737-698B-29	Sequence 29, Appl	C 216	14.2	64.5	115	4	US-09-270-767-2055	Sequence 2055, Appl
C 144	14.6	66.4	1890	4	US-09-270-767-10215	Sequence 10215, A	C 217	14.2	64.5	127	4	US-09-270-767-17337	Sequence 17337, A
C 145	14.6	66.4	2025	4	US-09-252-991A-14929	Sequence 14929, A	C 218	14.2	64.5	217	4	US-09-335-011-12	Sequence 12, Appl
C 146	14.6	66.4	2025	4	US-09-270-767-10213	Sequence 10213, A	C 219	14.2	64.5	221	4	US-09-313-994A-5438	Sequence 5438, Ap
C 147	14.6	66.4	2031	1	US-08-217-299-2	Sequence 2, Appl	C 220	14.2	64.5	221	4	US-09-313-994A-5438	Sequence 5438, Ap
C 148	14.6	66.4	2097	2	US-08-602-725-35	Sequence 35, Appl	C 221	14.2	64.5	342	3	US-08-638-931-51	Sequence 51, Appl
C 149	14.6	66.4	2220	1	US-08-389-459A-16	Sequence 16, Appl	C 222	14.2	64.5	348	3	US-08-638-931-57	Sequence 57, Appl
C 150	14.6	66.4	2220	3	US-08-967-867A-16	Sequence 16, Appl	C 223	14.2	64.5	349	3	US-08-638-931-55	Sequence 55, Appl
C 151	14.6	66.4	2349	2	US-08-184-009-145	Sequence 145, App	C 224	14.2	64.5	360	3	US-08-638-931-67	Sequence 67, Appl
C 152	14.6	66.4	2349	2	US-08-458-356-145	Sequence 145, App	C 225	14.2	64.5	362	3	US-08-638-931-52	Sequence 52, Appl
C 153	14.6	66.4	2349	4	US-08-460-736-145	Sequence 145, App	C 226	14.2	64.5	389	4	US-09-270-767-5338	Sequence 5338, Ap
C 154	14.6	66.4	2349	4	US-09-535-370-145	Sequence 145, App	C 227	14.2	64.5	389	4	US-09-270-767-20620	Sequence 20620, A
C 155	14.6	66.4	2349	4	US-09-663-667-145	Sequence 145, App	C 228	14.2	64.5	456	4	US-09-270-767-10950	Sequence 10950, A
C 156	14.6	66.4	2434	2	US-08-184-009-144	Sequence 144, App	C 229	14.2	64.5	461	4	US-09-679-409-47	Sequence 47, Appl
C 157	14.6	66.4	2434	2	US-08-458-356-144	Sequence 144, App	C 230	14.2	64.5	463	4	US-09-252-991A-6063	Sequence 6063, Ap
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C 159	14.6	66.4	2434	4	US-09-535-370-144	Sequence 144, App	C 232	14.2	64.5	483	4	US-09-270-767-24798	Sequence 24798, Ap
C 160	14.6	66.4	2434	4	US-09-663-667-144	Sequence 144, App	C 233	14.2	64.5	494	4	US-09-621-976-832	Sequence 832, App
C 161	14.6	66.4	2534	4	US-09-248-796A-5236	Sequence 5236, Ap	C 234	14.2	64.5	504	4	US-09-335-011-10	Sequence 10, Appl
C 162	14.6	66.4	2534	4	US-09-620-312D-80	Sequence 80, Appl	C 235	14.2	64.5	552	4	US-09-335-011-9	Sequence 9, Appl
C 163	14.6	66.4	2562	4	US-09-469-039A-5226	Sequence 5226, Ap	C 236	14.2	64.5	570	4	US-09-252-991A-777	Sequence 777, App
C 164	14.6	66.4	2818	4	US-09-415-161-14	Sequence 14, Appl	C 237	14.2	64.5	586	3	US-09-284-782-25	Sequence 25, Appl
C 165	14.6	66.4	2818	4	US-09-415-161-15	Sequence 15, Appl	C 238	14.2	64.5	617	4	US-09-539-333D-113	Sequence 113, App
C 166	14.6	66.4	2839	3	US-08-468-856B-5	Sequence 5, Appl	C 239	14.2	64.5	645	4	US-09-252-991A-4838	Sequence 4838, Ap
C 167	14.6	66.4	2839	3	US-08-468-859A-5	Sequence 5, Appl	C 240	14.2	64.5	696	4	US-09-149-476-92	Sequence 92, Appl
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 Patent No. 6725730  
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 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tunas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zhenli  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P33301C9  
 CURRENT APPLICATION NUMBER: US/10/140,002  
 PRIOR FILING DATE: 2002-05-06  
 PRIOR APPLICATION REMOVED - See Palm or File Wrapper  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 405  
 LENGTH: 3819  
 TYPE: DNA  
 ORGANISM: Homo Sapien

Sequence 792, App  
 Sequence 11, Appl  
 Sequence 9, Appl1  
 Sequence 16224, A  
 Sequence 14696, A  
 Sequence 4236, App  
 Sequence 113, App  
 Sequence 406, App  
 Sequence 432, App  
 Sequence 600, App  
 Sequence 11523, A  
 Sequence 1, Appl1  
 Sequence 723, App  
 Sequence 4440, App  
 Sequence 7057, App  
 Sequence 7125, App  
 Sequence 56, Appl  
 Sequence 2161, A  
 Sequence 10622, A  
 Sequence 438, App  
 Sequence 7728, App  
 Sequence 363, Appl  
 Sequence 1, Appl1  
 Sequence 367, App  
 Sequence 24, Appl  
 Sequence 11648, A  
 Sequence 274, App  
 Sequence 4168, App  
 Sequence 3, Appl1  
 Sequence 4643, App  
 Sequence 273, App  
 Sequence 667, App  
 Sequence 11561, A  
 Sequence 902, App



US-10-140-002-405

Query Match 95.5%; Score 21; DB 4; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGAGGTTCTCGATGAGAT 21  
Db 399 TCGAGGTTCTCGATGAGAT 379

RESULT 2

US-09-252-991A-10248  
; Sequence 10248, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10248  
; LENGTH: 441  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10248

Query Match 74.5%; Score 16.4; DB 4; Length 441;  
Best Local Similarity 94.4%; Pred. No. 89;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGGTTCTCGATGAG 19  
Db 274 TCGAGGTTCTCGATGAG 291

RESULT 3

US-09-252-991A-10461  
; Sequence 10461, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10461  
; LENGTH: 1659  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10461

Query Match 74.5%; Score 16.4; DB 4; Length 1659;  
Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGGTTCTCGATGAG 19  
Db 803 TCGAGGTTCTCGATGAG 820

RESULT 4

US-09-252-991A-10707/c  
; Sequence 10707, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10707  
; LENGTH: 3267  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10707

Query Match 74.5%; Score 16.4; DB 4; Length 3267;  
Best Local Similarity 94.4%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGGTTCTCGATGAG 19  
Db 758 TCGAGGTTCTCGATGAG 741

RESULT 5

US-09-252-991A-14488/c  
; Sequence 14488, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14488  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14488

Query Match 73.6%; Score 16.2; DB 4; Length 519;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAGGTTCTCGATGAGATC 22  
Db 234 TCGAGGTTCTCGGAGATC 214

RESULT 6

US-09-252-991A-15133  
; Sequence 15133, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15133  
LENGTH: 1347  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15133

Query Match 73.6%; Score 16.2; DB 4; Length 1347;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 788 TCGAGTTCTCGCGGAGATC 808

RESULT 7  
US-09-252-991A-14625/c  
Sequence 14625, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14625  
LENGTH: 1359  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14625

Query Match 73.6%; Score 16.2; DB 4; Length 1359;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 578 TCGAGTTCTCGCGGAGATC 558

RESULT 8  
US-09-252-991A-15137/c  
Sequence 15137, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15137  
LENGTH: 1446  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15137

Query Match 73.6%; Score 16.2; DB 4; Length 1446;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 1010 TCGAGTTCTCGAAGTCGATC 990

RESULT 9  
US-09-689-012-1/c  
Sequence 1, Application US/09689012  
Patent No. 6670135  
GENERAL INFORMATION:  
APPLICANT: Spri998, Melanie K.  
TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES  
FILE REFERENCE: 2634-US  
CURRENT APPLICATION NUMBER: US/09/689,012  
PRIOR FILING DATE: 2000-10-12  
PRIOR APPLICATION NUMBER: PCT/US99/09831  
PRIOR FILING DATE: 1999-05-05  
PRIOR APPLICATION NUMBER: US 60/085,497  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2001  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2001)  
OTHER INFORMATION:  
US-09-689-012-1

Query Match 73.6%; Score 16.2; DB 4; Length 2001;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGGAGAT 21  
DB 1575 TTCCGAGTTCTCGATGGAGAT 1555

RESULT 10  
US-09-240-410-1/c  
Sequence 1, Application US/09240410  
Patent No. 6197544  
GENERAL INFORMATION:  
APPLICANT: MICHALOVICH, DAVID  
APPLICANT: HAYES, PHILIP DAVID  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,410  
FILING DATE: 27-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK APPLICATION NO. TO BE ASSIGNED  
FILING DATE: 20-JAN-1999  
APPLICATION NUMBER: EP APPLICATION NO. 98300694.1

FILING DATE: 30-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-30039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0700  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2010 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-240-410-1

Query Match 73.6%; Score 16.2; DB 3; Length 2010;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 TTCGAGTCTCGATGAGAT 21  
|||||  
Db 1575 TTCGAGCTGTAGATGAGAT 1555

RESULT 11  
US-09-252-991A-14624  
; Sequence 14624, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14624  
; LENGTH: 2154  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14624

Query Match 73.6%; Score 16.2; DB 4; Length 2154;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 2 TTCGAGTCTCGATGAGATC 22  
|||||  
Db 482 TCGAGTCTCGAAGTCGATC 502

RESULT 12  
US-09-041-236-1/c  
; Sequence 1, Application US/09041236  
; Patent No. 6225285  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Yuling  
; APPLICANT: Xiomel, Xu  
; TITLE OF INVENTION: Semaphorin K1  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA

ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,236  
FILING DATE: March 11, 1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: EXEL98-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2498 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1902  
US-09-041-236-1

Query Match 73.6%; Score 16.2; DB 3; Length 2498;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 TTCGAGTCTCGATGAGAT 21  
|||||  
Db 1479 TTCGAGCTGTAGATGAGAT 1459

RESULT 13  
US-09-771-467C-1/c  
; Sequence 1, Application US/09771467C  
; Patent No. 6583277  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Yuling  
; APPLICANT: Xiomel, Xu  
; TITLE OF INVENTION: Semaphorin K1 Polypeptides  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/771,467C  
FILING DATE: 26-Jan-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: EXEL98-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2498 base pairs

```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1902
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-771-467C-1

Query Match      73.6%; Score 16.2; DB 4; Length 2498;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  TTGGAGTTCTCGATGAGATC 21
        |||||
Db      1479 TTGGAGCTGTATGATGAGAT 1459

RESULT 14
US-09-252-991A-15001/C
; Sequence 15001, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15001
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15001

Query Match      73.6%; Score 16.2; DB 4; Length 2622;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TCGAGTTCTCGATGAGATC 22
        |||||
Db      957  TCGAGTTCTCGATGAGATC 937

RESULT 15
US-09-669-751-133
; Sequence 133, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; TITLE OF INVENTION: Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669.751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-133

Query Match      71.8%; Score 15.8; DB 4; Length 550;
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```

;
; Best Local Similarity 89.5%; Pred. No. 1.8e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  TTGGAGTTCTCGATGAG 19
        |||||
Db      272 TTGGAGTTCTCGATGAGCG 290

RESULT 16
US-09-270-767-14247
; Sequence 14247, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14247
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14247

Query Match      71.8%; Score 15.8; DB 4; Length 636;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  TTGGAGTTCTCGATGAG 19
        |||||
Db      272 TTGGAGTTCTCGATGAGCG 290

RESULT 17
US-09-248-796A-414/C
; Sequence 414, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Ketch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 414
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-414

Query Match      71.8%; Score 15.8; DB 4; Length 744;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  GGAGTTCTCGATGAGATC 22
        |||||
Db      704 GGAGTTCTCGATGAGATC 686

RESULT 18
US-09-270-767-11307/C
; Sequence 11307, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```

FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11307  
LENGTH: 1586  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-11307

Query Match 71.8%; Score 15.8; DB 4; Length 1586;  
Best Local Similarity 89.5%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGATC 22  
DB 1315 GGCCTTCGATGATGATC 1297

RESULT 19  
US-09-252-991A-6042  
Sequence 6042, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6042  
LENGTH: 1836  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6042

Query Match 71.8%; Score 15.8; DB 4; Length 1836;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGATC 22  
DB 723 GGAGTTCGATGAGATC 741

RESULT 20  
US-09-252-991A-6258/C  
Sequence 6258, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6258  
LENGTH: 1911  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6258

Query Match 71.8%; Score 15.8; DB 4; Length 1911;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGATC 22  
DB 1156 GGAGTTCGATGAGATC 1138

RESULT 21  
US-09-016-434-320/C  
Sequence 320, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERBWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: 71-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 320:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: HMT3A2T01  
CLONE: 1854243  
US-09-016-434-320

Query Match 70.9%; Score 15.6; DB 4; Length 251;  
Best Local Similarity 81.8%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTGGAGTTCGATGAGATC 22  
DB 96 TTGGAGTTCGATGAGATC 75

RESULT 22  
US-09-328-352-3744  
Sequence 3744, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

```

; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3744
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3744

Query Match      70.9%; Score 15.6; DB 4; Length 393;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTTCGATGAGATC 22
DB      249 TTCAAGTTCGATGAGATC 270

RESULT 23
US-09-602-787A-199/c
; Sequence 199, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermann, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 199
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1072)
; OTHER INFORMATION: RXA02269
US-09-602-787A-199

Query Match      70.9%; Score 15.6; DB 4; Length 1095;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTTCGATGAGATC 22
DB      140 TTGGAGTTCGCGGAGATC 119

RESULT 24
US-09-492-709A-196/c
; Sequence 196, Application US/09492709A
; Patent No. 6720139
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001A
; CURRENT APPLICATION NUMBER: US/09/492,709A
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0

```

SEQ ID NO 196  
LENGTH: 1371  
TYPE: DNA  
ORGANISM: E. Coli  
US-09-492-709A-196

Query Match 70.9%; Score 15.6; DB 4; Length 1371;  
Best Local Similarity 81.8%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTTCGATGAGATC 22  
|||||  
Db 933 TTCGAGTTTCGATGAGATC 912  
|||||

RESULT 25  
US-09-799-875-3/c  
Sequence 3, Application US/09799875  
Patent No. 6638721

GENERAL INFORMATION:  
APPLICANT: Meyers, Rachel  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
TITLE OF INVENTION: Therefore  
FILE REFERENCE: 35800/209996  
CURRENT FILING DATE: 2001-03-06  
PRIOR APPLICATION NUMBER: 60/182,059  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/659,287  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 2637  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-799-875-3

Query Match 70.9%; Score 15.6; DB 4; Length 2637;  
Best Local Similarity 81.8%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTTCGATGAGATC 22  
|||||  
Db 2171 TTCGAGTTTCGATGAGATC 2150  
|||||

RESULT 26  
US-09-799-875-1/c  
Sequence 1, Application US/09799875  
Patent No. 6638721  
GENERAL INFORMATION:  
APPLICANT: Meyers, Rachel  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
TITLE OF INVENTION: Therefore  
FILE REFERENCE: 35800/209996  
CURRENT FILING DATE: US/09/799,875  
PRIOR APPLICATION NUMBER: 2001-03-06  
PRIOR FILING DATE: 60/182,059  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/659,287  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 3003  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: CDS  
LOCATION: (52)...(2688)  
US-09-799-875-1

Query Match 70.9%; Score 15.6; DB 4; Length 3003;  
Best Local Similarity 81.8%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTTCGATGAGATC 22  
|||||  
Db 2222 TTCGAGTTTCGATGAGATC 2201  
|||||

RESULT 27  
US-08-311-731A-123/c  
Sequence 123, Application US/08311731A  
Patent No. 6583266

GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36470 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULAR TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LAPRAE  
US-08-311-731A-123

Query Match 70.9%; Score 15.6; DB 4; Length 36470;  
Best Local Similarity 81.8%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTTCGATGAGATC 22  
|||||  
Db 17340 TACGTACTCCTCGATGAGATC 17319  
|||||

RESULT 28  
US-09-410-551B-1/c  
Sequence 1, Application US/09410551B  
Patent No. 6503737



```

; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTU, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Query Match          70.9%; Score 15.6; DB 4; Length 77536;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  TTGGAGTTCTCGATGGAGATC 22
DB      55028 TTGGCGATCTCGACGAGACC 55007

RESULT 29
US-09-940-316B-1/c
; Sequence 1, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTU, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-940-316B-1
```

```

Query Match          70.9%; Score 15.6; DB 4; Length 77536;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  TTGGAGTTCTCGATGGAGATC 22
DB      55028 TTGGCGATCTCGACGAGACC 55007

RESULT 30
US-09-799-451-327
; Sequence 327, Application US/09799451
; Patent No. 678369
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Rylye
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungding
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Drimnac, Radoje T.
; TITLE OF INVENTION: No. 678369e1 Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_FL_genes Version 2.0
; SEQ ID NO 327
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (355)..(1683)
US-09-799-451-327

Query Match          70.0%; Score 15.4; DB 4; Length 1686;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4  GGAGTTCTCGATGAGA 20
DB      1335 GGAGTTCTCGATGAGA 1351

RESULT 31
US-09-377-466B-9/c
; Sequence 9, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
OTHER INFORMATION: occurring nucleotide sequence encoding a Cry3Bb  
OTHER INFORMATION: variant 11231mw1 amino acid sequence  
NAME/KEY: CDS  
LOCATION: (3)..(1961)  
OTHER INFORMATION: coding sequence for a Cry3Bb variant 11231mw1  
OTHER INFORMATION: amino acid sequence  
US-09-377-466B-9

Query Match 70.0%; Score 15.4; DB 4; Length 1984;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGA 20  
DB 989 GGAGTTCGATGAGA 973

RESULT 32  
US-09-377-466B-11/c  
Sequence 11, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 1984  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
OTHER INFORMATION: occurring nucleotide sequence encoding a Cry3Bb  
OTHER INFORMATION: variant 11231mw2 amino acid sequence  
NAME/KEY: CDS  
LOCATION: (3)..(1961)  
OTHER INFORMATION: coding sequence for a Cry3Bb variant 11231mw2  
OTHER INFORMATION: amino acid sequence  
US-09-377-466B-11

Query Match 70.0%; Score 15.4; DB 4; Length 1984;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGA 20  
DB 989 GGAGTTCGATGAGA 973

RESULT 33  
US-09-377-466B-19/c  
Sequence 19, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 3039  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CamV.AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcd1  
NAME/KEY: Intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: CDS  
LOCATION: (811)..(2769)  
OTHER INFORMATION: Cry3Bb1 variant 11231mw1  
NAME/KEY: terminator  
LOCATION: (2787)..(3020)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-19

Query Match 70.0%; Score 15.4; DB 4; Length 3039;  
Best Local Similarity 94.1%; Pred. No. 3.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGA 20  
DB 1797 GGAGTTCGATGAGA 1781

RESULT 34  
US-09-377-466B-21/c  
Sequence 21, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 21  
LENGTH: 3039  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CamV.AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcd1  
NAME/KEY: Intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: CDS  
LOCATION: (811)..(2769)  
OTHER INFORMATION: Cry3Bb1 variant 11231mw2  
NAME/KEY: terminator  
LOCATION: (2787)..(3020)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-21

Query Match 70.0%; Score 15.4; DB 4; Length 3039;  
Best Local Similarity 94.1%; Pred. No. 3.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTCGATGAGA 20  
DB 1797 GGAGTTCGATGAGA 1781

RESULT 35  
US-09-377-466B-17/c

```
Sequence 17, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3450
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: Promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: transic peptide
LOCATION: (825)..(971)
OTHER INFORMATION: amino terminal TS-Zm.rbcs
NAME/KEY: Intron
LOCATION: (972)..(1134)
OTHER INFORMATION: I-Zm.rbcs
NAME/KEY: transic peptide
LOCATION: (1135)..(1221)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
NAME/KEY: CDS
LOCATION: (1222)..(3180)
OTHER INFORMATION: Cry3Bb1 variant 11231mv1
NAME/KEY: terminator
LOCATION: (3198)..(3431)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-17

Query Match          70.0%; Score 15.4; DB 4; Length 3450;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 GGAGTTCTCGATGAGA 20
Db 2208 GGAGTTCTCGATGACA 2192

RESULT 36
US-09-377-466B-23/c
Sequence 23, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: Promoter
LOCATION: (25)..(640)
```

```
OTHER INFORMATION: P-CaMV.J5S
NAME/KEY: 5'UTR
LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (748)..(1238)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bb1 variant 11231mv2
NAME/KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-23

Query Match          70.0%; Score 15.4; DB 4; Length 3469;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 GGAGTTCTCGATGAGA 20
Db 2227 GGAGTTCTCGATGACA 2211

RESULT 37
US-08-637-759B-8/c
Sequence 8, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPLMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Partial sequence of Salmonella typhimurium
US-08-637-759B-8
```

Query Match 69.1%; Score 15.2; DB 2; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

## RESULT 38

US-08-871-355A-8/c  
; Sequence 8, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPLMS 101 CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Partial sequence of *Salmonella typhimurium*  
; ORGANISM: virulence gene  
US-08-871-355A-8

Query Match 69.1%; Score 15.2; DB 3; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

RESULT 39  
US-09-201-945-8/c  
; Sequence 8, Application US/09201945  
; Patent No. 6342215

GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,945  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/637,759  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPLMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8795  
; TELEFAX: (404) 873-8794  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Partial sequence of *Salmonella typhimurium*  
; ORGANISM: virulence gene  
US-09-201-945-8

Query Match 69.1%; Score 15.2; DB 3; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

RESULT 40  
US-09-621-976-15382/c  
; Sequence 15382, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 15382  
; LENGTH: 413  
; TYPE: DNA  
; ORGANISM: *Homo sapiens*

US-09-621-976-15382

Query Match 69.1%; Score 15.2; DB 4; Length 413;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 389 TTGGCAGTTCTCGAAGAGAGA 370

RESULT 41  
US-09-513-999C-12831/C  
Sequence 12831, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 12831  
LENGTH: 565  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 391  
OTHER INFORMATION: m=a or c  
US-09-513-999C-12831

Query Match 69.1%; Score 15.2; DB 4; Length 565;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

RESULT 42  
US-09-270-767-2463/C  
Sequence 2463, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2463  
LENGTH: 621  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-2463

Query Match 69.1%; Score 15.2; DB 4; Length 621;  
Best Local Similarity 85.0%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGATTCTCGATGAGATC 22  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

DB 470 CGGACTTCTCGATCGGAGATC 451

RESULT 43  
US-09-270-767-17745/C  
Sequence 17745, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 17745  
LENGTH: 621  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-17745

Query Match 69.1%; Score 15.2; DB 4; Length 621;  
Best Local Similarity 85.0%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGTTCTCGATGAGATC 22  
DB 470 CGGACTTCTCGATCGGAGATC 451

RESULT 44  
US-09-513-999C-1940/C  
Sequence 1940, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 1940  
LENGTH: 690  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 310..690  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 508  
OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: UNSURB  
LOCATION: 67  
OTHER INFORMATION: Xaa=Asp or His or Asn or Tyr  
US-09-513-999C-1940

Query Match 69.1%; Score 15.2; DB 4; Length 690;  
Best Local Similarity 85.0%; Pred. No. 3.6e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

RESULT 45  
US-09-602-787A-61  
Sequence 61, Application US/09602787A  
Patent No. 6696561  
GENERAL INFORMATION:  
APPLICANT: Pompeius, Mark  
APPLICANT: Krüger, Burthard  
APPLICANT: Schöder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Habeshauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
TRANSPORT  
FILE REFERENCE: BGI-125CP  
CURRENT APPLICATION NUMBER: US/09/602,787A  
CURRENT FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: USN 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: DE 19931454.3  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931478.0  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931563.9  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932122.1  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932124.8  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932125.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932128.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932180.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932182.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932190.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932191.4  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932209.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932212.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932227.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932228.7  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932229.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932230.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932927.3  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933005.0  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933006.9  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19940764.9  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940765.7  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940766.5  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940830.0  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940831.9  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940832.7  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940833.5

PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19941378.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941395.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19942077.7  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942078.5  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942079.3  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942088.2  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 678  
SEQ ID NO 61  
LENGTH: 1047  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (101)..(1024)  
OTHER INFORMATION: RXA01060  
US-09-602-787A-61

Query Match 69.1%; Score 15.2; DB 4; Length 1047;  
Best Local Similarity 85.0%; Pred. No. 3.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGTCTCGATCGAGATC 22  
DB 643 CGGAGATCTGATCGAGATC 662

RESULT 46  
US-09-146-675-2  
Sequence 2, Application US/09146675B  
Patent No. 6048731  
GENERAL INFORMATION:  
APPLICANT: Kong, Huijun  
APPLICANT: Higgins S., Lauren  
APPLICANT: Dalton A., Michael  
TITLE OF INVENTION: Method For Cloning And Producing The SgrAI Restriction  
FILE REFERENCE: SgrAI  
CURRENT APPLICATION NUMBER: US/09/146,675B  
CURRENT FILING DATE: 1998-09-03  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1290  
TYPE: DNA  
ORGANISM: Streptomyces griseus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1287)  
US-09-146-675-2

Query Match 69.1%; Score 15.2; DB 3; Length 1290;  
Best Local Similarity 85.0%; Pred. No. 4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATCGAGA 20  
DB 592 TTCGCGCTTCGCGATGGGA 611

RESULT 47  
US-09-252-991A-9857/C  
Sequence 9857, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9857  
LENGTH: 1722  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9857

Query Match 69.1%; Score 15.2; DB 4; Length 1722;  
Best Local Similarity 85.0%; Pred. No. 4.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGAGAT 21  
DB 1616 TCGCGCATCTCGATGAGATT 1597

RESULT 48  
US-09-548-938A-4/C  
Sequence 4, Application US/09548938A  
Patent No. 6573086  
GENERAL INFORMATION:  
APPLICANT: EMALFARB, MARK AARON  
APPLICANT: BURLINGAME, RICHARD PAUL  
APPLICANT: OLSON, PHILIP TERRY  
APPLICANT: SINITSYN, ARKADY PANTELEIMONOVICH  
APPLICANT: BOUSSON, JEAN CHRISTOPHE  
APPLICANT: PARNONEN, CHRISTINE MARIE  
APPLICANT: PUNT, PETER JAN  
APPLICANT: VAN-ZEIJL, CORNELIA MARIA JOHANNA  
TITLE OF INVENTION: TRANSFORMATION SYSTEM IN THE FIELD OF FILAMENTOUS FUNGI  
FILE REFERENCE: 3123-4001  
CURRENT APPLICATION NUMBER: US/09/548,938A  
CURRENT FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 2547  
TYPE: DNA  
ORGANISM: Chrysosporium lucknowense  
US-09-548-938A-4

Query Match 69.1%; Score 15.2; DB 4; Length 2547;  
Best Local Similarity 85.0%; Pred. No. 4.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGAGAT 21  
DB 1632 TCGAGTGTCTCGATGAGATT 1613

RESULT 49  
US-09-112-580-5/C  
Sequence 5, Application US/09112580  
Patent No. 6610539  
GENERAL INFORMATION:  
APPLICANT: WRIGHT, Jim A.  
APPLICANT: YOUNG, Aiding  
APPLICANT: DUGOURD, Dominique  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF  
FILE REFERENCE: 032396-016  
CURRENT APPLICATION NUMBER: US/09/112,580

CURRENT FILING DATE: 1998-07-09  
EARLIER APPLICATION NUMBER: US 60/052,160  
EARLIER FILING DATE: 1997-07-10  
NUMBER OF SEQ ID NOS: 265  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 3811  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-112-580-5

Query Match 69.1%; Score 15.2; DB 4; Length 3811;  
Best Local Similarity 85.0%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGAGAT 21  
DB 2209 TCGATTCTTCGATGAGAT 2190

RESULT 50  
US-09-302-626B-59/C  
Sequence 59, Application US/09302626B  
Patent No. 6709660  
GENERAL INFORMATION:  
APPLICANT: Scalato, Enzo  
APPLICANT: Maignani, Vega  
APPLICANT: Rappuoli, Rino  
APPLICANT: Pizzi, Mariagrazia  
APPLICANT: Grandi, Guido  
TITLE OF INVENTION: Meningococcal Antigens  
FILE REFERENCE: CHIR0159  
CURRENT APPLICATION NUMBER: US/09/302,626B  
CURRENT FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: PCT/IB99/00103  
PRIOR FILING DATE: 1999-01-14  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 5937  
TYPE: DNA  
ORGANISM: Neisseria meningitidis  
US-09-302-626B-59

Query Match 69.1%; Score 15.2; DB 4; Length 5937;  
Best Local Similarity 85.0%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGAGTTCTCGATGAGA 20  
DB 1044 TTCGATGTTTCGATGAGA 1025

Search completed: February 2, 2005, 01:35:44  
Job time : 112 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 23:49:03 ; Search time 418 Seconds

(without alignments)  
302.415 Million cell updates/sec

Title: US-10-073-054-14

Perfect score: 22

Sequence: 1 ttcgagagcttcgagatgcagatc 22

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues 8600550

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

## Database :

Published Applications NA.\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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21: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	22	15	US-10-073-054-14	Sequence 14, Appl
2	95.5	22	15	US-10-073-054-11	Sequence 11, Appl
3	95.5	423	9	US-09-864-761-25383	Sequence 25383, A
4	95.5	493	10	US-09-814-353-14450	Sequence 14450, A
5	95.5	527	18	US-10-723-860-3391	Sequence 3391, Ap
6	95.5	582	9	US-09-864-761-8712	Sequence 8712, Ap
7	95.5	2061	9	US-09-529-063-74	Sequence 74, Appl
8	95.5	2061	13	US-10-414-376-74	Sequence 14, Appl
9	95.5	2231	13	US-10-011-370-1	Sequence 1, Appl
10	95.5	2816	15	US-10-073-054-5	Sequence 5, Appl
11	95.5	2821	15	US-10-295-027-767	Sequence 767, App
12	95.5	2822	9	US-09-845-771-1	Sequence 1, Appl

13	95.5	2822	15	US-10-225-567A-517	Sequence 517, App
14	95.5	2822	15	US-10-073-054-1	Sequence 1, Appl
15	95.5	2822	15	US-10-460-479-1	Sequence 1, Appl
16	95.5	2824	17	US-10-322-281-337	Sequence 337, App
17	95.5	2824	17	US-10-322-281-339	Sequence 339, App
18	95.5	3564	9	US-09-529-063-75	Sequence 75, Appl
19	95.5	3564	15	US-10-414-378-75	Sequence 75, Appl
20	95.5	3686	15	US-10-263-230A-8	Sequence 8, Appl
21	95.5	3711	15	US-10-073-054-3	Sequence 3, Appl
22	95.5	3711	15	US-10-328-544-1	Sequence 1, Appl
23	95.5	3789	17	US-10-322-281-335	Sequence 335, App
24	95.5	3819	9	US-09-978-295A-482	Sequence 482, App
25	95.5	3819	9	US-09-978-697-482	Sequence 482, App
26	95.5	3819	9	US-09-978-192A-482	Sequence 482, App
27	95.5	3819	9	US-09-999-832A-482	Sequence 482, App
28	95.5	3819	10	US-09-978-189-482	Sequence 482, App
29	95.5	3819	10	US-09-978-608A-482	Sequence 482, App
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31	95.5	3819	10	US-09-978-191A-482	Sequence 482, App
32	95.5	3819	10	US-09-978-403A-482	Sequence 482, App
33	95.5	3819	10	US-09-978-564A-482	Sequence 482, App
34	95.5	3819	10	US-09-999-833A-482	Sequence 482, App
35	95.5	3819	10	US-09-981-915A-482	Sequence 482, App
36	95.5	3819	10	US-09-978-824-482	Sequence 482, App
37	95.5	3819	10	US-09-918-583A-482	Sequence 482, App
38	95.5	3819	10	US-09-999-834A-482	Sequence 482, App
39	95.5	3819	10	US-09-978-423A-482	Sequence 482, App
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44	95.5	3819	10	US-09-978-643A-482	Sequence 482, App
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53	95.5	3819	10	US-09-978-665A-482	Sequence 482, App
54	95.5	3819	10	US-09-978-802A-482	Sequence 482, App
55	95.5	3819	11	US-09-999-831A-482	Sequence 482, App
56	95.5	3819	14	US-10-028-072-405	Sequence 405, App
57	95.5	3819	14	US-10-140-806-405	Sequence 405, App
58	95.5	3819	14	US-10-121-049-405	Sequence 405, App
59	95.5	3819	14	US-10-123-904-405	Sequence 405, App
60	95.5	3819	14	US-10-140-476-405	Sequence 405, App
61	95.5	3819	14	US-10-142-431-405	Sequence 405, App
62	95.5	3819	14	US-10-143-114-405	Sequence 405, App
63	95.5	3819	14	US-10-176-921-405	Sequence 405, App
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65	95.5	3819	14	US-10-137-865-405	Sequence 405, App
66	95.5	3819	14	US-10-140-476-405	Sequence 405, App
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68	95.5	3819	14	US-10-143-114-405	Sequence 405, App
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72	95.5	3819	14	US-10-218-631-133	Sequence 133, App
73	95.5	3819	14	US-10-017-081A-482	Sequence 482, App
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75	95.5	3819	14	US-10-142-423-405	Sequence 405, App
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C 88	21	95.5	3819	14	US-10-140-928-405	Sequence 405, App	C 161	21	95.5	3819	14	US-10-146-729-405	Sequence 405, App
C 89	21	95.5	3819	14	US-10-216-159A-483	Sequence 133, App	C 162	21	95.5	3819	14	US-10-146-791-405	Sequence 405, App
C 90	21	95.5	3819	14	US-10-013-929A-482	Sequence 482, App	C 163	21	95.5	3819	14	US-10-147-84-405	Sequence 405, App
C 91	21	95.5	3819	14	US-10-016-177A-482	Sequence 482, App	C 164	21	95.5	3819	14	US-10-147-512-405	Sequence 405, App
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C 107	21	95.5	3819	14	US-10-127-901A-405	Sequence 405, App	C 180	21	95.5	3819	14	US-10-127-822A-405	Sequence 405, App
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C 126	21	95.5	3819	14	US-10-123-902-405	Sequence 405, App	C 199	21	95.5	3819	14	US-10-230-017-405	Sequence 405, App
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C 239	21	95.5	3819	14	US-10-232-224-133	Sequence 133, App	C 312	21	95.5	3819	15	US-10-147-826-405	Sequence 405, App
C 240	21	95.5	3819	15	US-10-219-060-133	Sequence 133, App	C 313	21	95.5	3819	15	US-10-147-870-405	Sequence 405, App
C 241	21	95.5	3819	15	US-10-123-912-405	Sequence 405, App	C 314	21	95.5	3819	15	US-10-147-876-405	Sequence 405, App
C 242	21	95.5	3819	15	US-10-223-085-91	Sequence 91, App1	C 315	21	95.5	3819	15	US-10-147-959-405	Sequence 405, App
C 243	21	95.5	3819	15	US-10-216-160-133	Sequence 133, App	C 316	21	95.5	3819	15	US-10-147-724-405	Sequence 405, App
C 244	21	95.5	3819	15	US-10-216-162-133	Sequence 133, App	C 317	21	95.5	3819	15	US-10-146-725-405	Sequence 405, App
C 245	21	95.5	3819	15	US-10-216-164-133	Sequence 133, App	C 318	21	95.5	3819	15	US-10-146-775-405	Sequence 405, App
C 246	21	95.5	3819	15	US-10-216-167-133	Sequence 133, App	C 319	21	95.5	3819	15	US-10-147-495-405	Sequence 405, App
C 247	21	95.5	3819	15	US-10-216-168-133	Sequence 133, App	C 320	21	95.5	3819	15	US-10-147-501-405	Sequence 405, App
C 248	21	95.5	3819	15	US-10-219-065-133	Sequence 133, App	C 321	21	95.5	3819	15	US-10-147-504-405	Sequence 405, App
C 249	21	95.5	3819	15	US-10-219-071-133	Sequence 133, App	C 322	21	95.5	3819	15	US-10-147-506-405	Sequence 405, App
C 250	21	95.5	3819	15	US-10-219-074-133	Sequence 133, App	C 323	21	95.5	3819	15	US-10-147-510-405	Sequence 405, App
C 251	21	95.5	3819	15	US-10-219-077-133	Sequence 133, App	C 324	21	95.5	3819	15	US-10-147-511-405	Sequence 405, App
C 252	21	95.5	3819	15	US-10-219-465-133	Sequence 133, App	C 325	21	95.5	3819	15	US-10-147-559-405	Sequence 405, App
C 253	21	95.5	3819	15	US-10-219-467-133	Sequence 133, App	C 326	21	95.5	3819	15	US-10-157-397-405	Sequence 405, App
C 254	21	95.5	3819	15	US-10-219-469-133	Sequence 133, App	C 327	21	95.5	3819	15	US-10-153-386-405	Sequence 405, App
C 255	21	95.5	3819	15	US-10-219-471-133	Sequence 133, App	C 328	21	95.5	3819	15	US-10-153-786-405	Sequence 405, App
C 256	21	95.5	3819	15	US-10-219-473-133	Sequence 133, App	C 329	21	95.5	3819	15	US-10-158-766-405	Sequence 405, App
C 257	21	95.5	3819	15	US-10-219-476-133	Sequence 133, App	C 330	21	95.5	3819	15	US-10-143-031A-482	Sequence 482, App
C 258	21	95.5	3819	15	US-10-219-482-133	Sequence 133, App	C 331	21	95.5	3819	15	US-10-137-870-405	Sequence

C 378	21	95.5	3819	15	US-10-145-747-405	Sequence 405, App
C 379	21	95.5	3819	15	US-10-145-752-405	Sequence 405, App
C 380	21	95.5	3819	15	US-10-145-754-405	Sequence 405, App
C 381	21	95.5	3819	15	US-10-145-755-405	Sequence 405, App
C 382	21	95.5	3819	15	US-10-145-818-405	Sequence 405, App
C 383	21	95.5	3819	15	US-10-145-820-405	Sequence 405, App
C 384	21	95.5	3819	15	US-10-145-872-405	Sequence 405, App
C 385	21	95.5	3819	15	US-10-145-873-405	Sequence 405, App
C 386	21	95.5	3819	15	US-10-147-481-405	Sequence 405, App
C 387	21	95.5	3819	15	US-10-147-482-405	Sequence 405, App
C 388	21	95.5	3819	15	US-10-147-503-405	Sequence 405, App
C 389	21	95.5	3819	15	US-10-147-522-405	Sequence 405, App
C 390	21	95.5	3819	15	US-10-152-401-405	Sequence 405, App
C 391	21	95.5	3819	15	US-10-157-783-405	Sequence 405, App
C 392	21	95.5	3819	15	US-10-158-792-405	Sequence 405, App
C 393	21	95.5	3819	15	US-10-158-792-405	Sequence 405, App
C 394	21	95.5	3819	15	US-10-143-035-405	Sequence 405, App
C 395	21	95.5	3819	15	US-10-145-751-405	Sequence 405, App
C 396	21	95.5	3819	15	US-10-145-822-405	Sequence 405, App
C 397	21	95.5	3819	15	US-10-145-824-405	Sequence 405, App
C 398	21	95.5	3819	15	US-10-145-827-405	Sequence 405, App
C 399	21	95.5	3819	15	US-10-145-869-405	Sequence 405, App
C 400	21	95.5	3819	15	US-10-145-875-405	Sequence 405, App
C 401	21	95.5	3819	15	US-10-145-877-405	Sequence 405, App
C 402	21	95.5	3819	15	US-10-145-877-405	Sequence 405, App
C 403	21	95.5	3819	15	US-10-146-787-405	Sequence 405, App
C 404	21	95.5	3819	15	US-10-146-790-405	Sequence 405, App
C 405	21	95.5	3819	15	US-10-146-793-405	Sequence 405, App
C 406	21	95.5	3819	15	US-10-147-480-405	Sequence 405, App
C 407	21	95.5	3819	15	US-10-147-485-405	Sequence 405, App
C 408	21	95.5	3819	15	US-10-147-486-405	Sequence 405, App
C 409	21	95.5	3819	15	US-10-147-487-405	Sequence 405, App
C 410	21	95.5	3819	15	US-10-147-490-405	Sequence 405, App
C 411	21	95.5	3819	15	US-10-147-494-405	Sequence 405, App
C 412	21	95.5	3819	15	US-10-147-498-405	Sequence 405, App
C 413	21	95.5	3819	15	US-10-147-514-405	Sequence 405, App
C 414	21	95.5	3819	15	US-10-147-524-405	Sequence 405, App
C 415	21	95.5	3819	15	US-10-152-379-405	Sequence 405, App
C 416	21	95.5	3819	15	US-10-152-394-405	Sequence 405, App
C 417	21	95.5	3819	15	US-10-152-406-405	Sequence 405, App
C 418	21	95.5	3819	15	US-10-156-847-405	Sequence 405, App
C 419	21	95.5	3819	15	US-10-157-778-405	Sequence 405, App
C 420	21	95.5	3819	15	US-10-157-799-405	Sequence 405, App
C 421	21	95.5	3819	15	US-10-160-504-405	Sequence 405, App
C 422	21	95.5	3819	15	US-10-017-191A-482	Sequence 482, App
C 423	21	95.5	3819	15	US-10-145-634-405	Sequence 405, App
C 424	21	95.5	3819	15	US-10-147-520-405	Sequence 405, App
C 425	21	95.5	3819	15	US-10-157-781-405	Sequence 405, App
C 426	21	95.5	3819	15	US-10-156-889-405	Sequence 405, App
C 427	21	95.5	3819	15	US-10-147-491-405	Sequence 405, App
C 428	21	95.5	3819	15	US-10-152-378-405	Sequence 405, App
C 429	21	95.5	3819	15	US-10-152-382-405	Sequence 405, App
C 430	21	95.5	3819	15	US-10-152-383-405	Sequence 405, App
C 431	21	95.5	3819	15	US-10-152-384-405	Sequence 405, App
C 432	21	95.5	3819	15	US-10-152-387-405	Sequence 405, App
C 433	21	95.5	3819	15	US-10-152-389-405	Sequence 405, App
C 434	21	95.5	3819	15	US-10-152-390-405	Sequence 405, App
C 435	21	95.5	3819	15	US-10-152-392-405	Sequence 405, App
C 436	21	95.5	3819	15	US-10-152-403-405	Sequence 405, App
C 437	21	95.5	3819	15	US-10-153-756-405	Sequence 405, App
C 438	21	95.5	3819	15	US-10-157-784-405	Sequence 405, App
C 439	21	95.5	3819	15	US-10-157-797-405	Sequence 405, App
C 440	21	95.5	3819	15	US-10-158-491-405	Sequence 405, App
C 441	21	95.5	3819	15	US-10-143-028A-482	Sequence 482, App
C 442	21	95.5	3819	15	US-10-143-028A-482	Sequence 482, App
C 443	21	95.5	3819	15	US-10-142-762-405	Sequence 405, App
C 444	21	95.5	3819	15	US-10-142-764-405	Sequence 405, App
C 445	21	95.5	3819	15	US-10-142-766-405	Sequence 405, App
C 446	21	95.5	3819	15	US-10-145-089A-482	Sequence 482, App
C 447	21	95.5	3819	15	US-10-145-625-405	Sequence 405, App
C 448	21	95.5	3819	15	US-10-145-627-405	Sequence 405, App
C 449	21	95.5	3819	15	US-10-145-960-405	Sequence 405, App
C 450	21	95.5	3819	15	US-10-145-962-405	Sequence 405, App

RESULT 1  
US-10-073-054-14  
; Sequence 14, Application US/10073054  
; Publication No. US20030167485A1  
GENERAL INFORMATION:  
; APPLICANT: Garvan Institute of Medical Research  
; APPLICANT: HERCOC, Herbert  
; TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding gene  
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
; CURRENT APPLICATION NUMBER: US/10/073,054  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US 09/308,696  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00805  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: AU P09386  
; PRIOR FILING DATE: 1997-09-24

NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 14  
LENGTH: 22  
TYPE: DNA  
ORGANISM: probe  
US-10-073-054-14

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0;

Qy 1 TTCGAGTTCGATGAGATC 22  
Db 1 TTCGAGTTCGATGAGATC 22

RESULT 2  
US-10-073-054-11/c

Sequence 11, Application US/10073054  
Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: Gartner Institute of Medical Research  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: the G-protein coupled receptor-encoding gene an

FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
CURRENT APPLICATION NUMBER: US/10/073,054  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: US 09/308,696  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 11  
LENGTH: 22  
TYPE: DNA  
ORGANISM: probe  
US-10-073-054-11

Query Match 95.5%; Score 21; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 22 TTCGAGTTCGATGAGAT 22

RESULT 3  
US-09-864-761-25383/c

Sequence 25383, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aeonica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6

Query Match 95.5%; Score 21; DB 9; Length 423;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO: 25383  
LENGTH: 423  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC018552.2  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.4  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2  
OTHER INFORMATION: EXPRESSED IN P28984, EVALUATE 3.70e-01  
OTHER INFORMATION: NT HIT: AJ011001.1, EVALUATE 0.00e+00  
OTHER INFORMATION: EST\_HUMAN HIT: AL046540.1, EVALUATE 0.00e+00  
US-09-864-761-25383

Query Match 95.5%; Score 21; DB 9; Length 423;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 122 TTCGAGTTCGATGAGAT 102

RESULT 4  
US-09-814-353-14450/c

Sequence 14450, Application US/09814353  
Publication No. US20030165831A1  
GENERAL INFORMATION:  
APPLICANT: Lee, John  
APPLICANT: Thompson, Pamela  
APPLICANT: Lillie, James  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF OVARIAN CANCER  
FILE REFERENCE: MRI-0068  
CURRENT APPLICATION NUMBER: US/09/814,353  
CURRENT FILING DATE: 2001-03-21

Query Match 95.5%; Score 21; DB 9; Length 423;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

PRIOR APPLICATION NUMBER: US 60/191,031  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/251,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14450  
LENGTH: 493  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-814-353-14450

Query Match 95.5%; Score 21; DB 10; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGAGTTCTCGATGAGAT 21  
DB 416 TTCGGAGTTCTCGATGAGAT 396

RESULT 5  
US-10-723-860-3391/c  
Sequence 3391, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natascha  
APPLICANT: Zlotnick, Albert M.  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3391  
LENGTH: 527  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-723-860-3391

Query Match 95.5%; Score 21; DB 18; Length 527;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGAGTTCTCGATGAGAT 21  
DB 247 TTCGGAGTTCTCGATGAGAT 227

RESULT 6  
US-09-864-761-8712/c  
Sequence 8712, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
SEQ ID NO 8712  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC018552.2  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.4  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2  
US-09-864-761-8712

Query Match 95.5%; Score 21; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGAGTTCTCGATGAGAT 21  
DB 227 TTCGGAGTTCTCGATGAGAT 207

RESULT 7  
US-09-529-063-74/c  
Sequence 74, Application US/09529063  
Patent No. US20020102542A1  
GENERAL INFORMATION:  
APPLICANT: FUKUSHIMA, DAICHI  
APPLICANT: SHIBAYAMA, SHIRO  
APPLICANT: TADA, HIDEAKI

FILE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
TITLE OF INVENTION: THE BOTH  
FILE REFERENCE: 058769  
CURRENT APPLICATION NUMBER: US/09/529,063  
CURRENT FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: PCT/JP98/04514  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 74  
LENGTH: 2061  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-529-063-74

Query Match 95.5%; Score 21; DB 9; Length 2061;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 186 TTCGAGTTCTCGATGAGAT 166

RESULT 8  
US-10-414-378-74/c  
Sequence 74, Application US/10414378  
Publication No. US20030165981A1  
GENERAL INFORMATION:  
APPLICANT: FUKUSHIMA, DAIKICHI  
APPLICANT: SHIBAYAMA, SHIRO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
FILE REFERENCE: THE BOTH  
FILE REFERENCE: 058769  
CURRENT APPLICATION NUMBER: US/10/414,378  
CURRENT FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: US/09/529,063  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: PCT/JP98/04514  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 74  
LENGTH: 2061  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-414-378-74

Query Match 95.5%; Score 21; DB 15; Length 2061;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 186 TTCGAGTTCTCGATGAGAT 166

RESULT 9  
US-10-011-370-1/c  
Sequence 1, Application US/10011370  
Publication No. US20020151704A1  
GENERAL INFORMATION:  
APPLICANT: Borowsky, Beth E.  
APPLICANT: Ogozalek, Kristine L.  
APPLICANT: Kyaw, Hla  
APPLICANT: Pathirana, Marie Sudam  
APPLICANT: Smith, Kelli E.  
TITLE OF INVENTION: DNA Encoding Orphan SNORF10 Receptor

FILE REFERENCE: 58988  
CURRENT APPLICATION NUMBER: US/10/011,370  
CURRENT FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US/09/286,085  
PRIOR FILING DATE: 1999-04-05  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.0 - beta  
SEQ ID NO 1  
LENGTH: 2231  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-011-370-1

Query Match 95.5%; Score 21; DB 13; Length 2231;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 258 TTCGAGTTCTCGATGAGAT 238

RESULT 10  
US-10-073-054-5/c  
Sequence 5, Application US/10073054  
Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: Garvan Institute of Medical Research  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: NO. US20030167485A1 G-protein coupled receptor-encoding gene  
FILE REFERENCE: 1871-132 (93702-CIP/WRO)  
CURRENT APPLICATION NUMBER: US/10/073,054  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: US 09/308,596  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 5  
LENGTH: 2816  
TYPE: DNA  
ORGANISM: human GPR56-3  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (159)..(2237)  
OTHER INFORMATION:  
US-10-073-054-5

Query Match 95.5%; Score 21; DB 15; Length 2816;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 344 TTCGAGTTCTCGATGAGAT 324

RESULT 11  
US-10-295-027-767/c  
Sequence 767, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afari, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.







PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 75  
LENGTH: 3564  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: (43)..(2103)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (118)..(2103)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (43)..(2103)  
US-10-414-378-75

Query Match 95.5%; Score 21; DB 15; Length 3564;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
|||||  
DB 228 TTCGAGTTCTCGATGAGAT 208

RESULT 20  
US-10-263-230A-8/C  
Sequence 8, Application US/10263230A  
Publication No. US20030152963A1  
GENERAL INFORMATION:  
APPLICANT: Duhl, David  
TITLE OF INVENTION: Gorman, Susan Wilkie  
TITLE OF INVENTION: HUMAN CHROMOSOME 15 AND 16 BARDST-BLEDI.  
FILE REFERENCE: 59516-243/PP-1568.002  
CURRENT FILING DATE: 2002-10-02  
CURRENT APPLICATION NUMBER: US/10/263,230A  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 3686  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-263-230A-8

Query Match 95.5%; Score 21; DB 15; Length 3686;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
|||||  
DB 318 TTCGAGTTCTCGATGAGAT 298

RESULT 21  
US-10-073-054-3/C  
Sequence 3, Application US/10073054  
Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: Gargan Institute of Medical Research  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: NO. US20030167485A1 G-protein coupled receptor-encoding gene an  
FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
CURRENT FILING DATE: 2002-02-12  
CURRENT APPLICATION NUMBER: US/10/073,054  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805

PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 3  
LENGTH: 3711  
TYPE: DNA  
ORGANISM: human GPR56-2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (168)..(2246)  
OTHER INFORMATION:  
US-10-073-054-3

Query Match 95.5%; Score 21; DB 15; Length 3711;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
|||||  
DB 353 TTCGAGTTCTCGATGAGAT 333

RESULT 22  
US-10-328-544-1/C  
Sequence 1, Application US/10328544  
Publication No. US20030175209A1  
GENERAL INFORMATION:  
APPLICANT: MUELLER, SABINE  
APPLICANT: GONZALEZ-ZULIETA, MIRELLA  
APPLICANT: FOHR, ERIC  
TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION  
FILE REFERENCE: AGT-008051  
CURRENT FILING DATE: 2002-12-23  
CURRENT APPLICATION NUMBER: US/10/328,544  
PRIOR FILING DATE: 2001-12-27  
PRIOR APPLICATION NUMBER: 60/343,422  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 1  
LENGTH: 3711  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (168)..(2249)  
OTHER INFORMATION:  
US-10-328-544-1

Query Match 95.5%; Score 21; DB 15; Length 3711;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
|||||  
DB 353 TTCGAGTTCTCGATGAGAT 333

RESULT 23  
US-10-322-281-335/C  
Sequence 335, Application US/10322281  
Publication No. US20040126762A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
APPLICANT: Marc S. Malandino  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001000  
CURRENT FILING DATE: 2002-12-17  
CURRENT APPLICATION NUMBER: US/10/322,281  
NUMBER OF SEQ ID NOS: 866  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 335  
LENGTH: 3789  
TYPE: DNA  
ORGANISM: Homo sapiens  
us-10-322-281-335

Query Match 95.5%; Score 21; DB 17; Length 3789;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 333 TTCGAGTTCGATGAGAT 313

RESULT 24  
US-09-978-295A-482/c  
Sequence 482, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoves, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kiljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
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PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085523  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 9; Length 3819;

Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTCTCGATGAGAT 21  
DB 399 TTGGAGTCTCGATGAGAT 379

## RESULT 25

US-09-978-697-482/c

Sequence 482, Application US/0978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijaviri, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James J.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697

PRIOR FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886

PRIOR FILING DATE: 1998-03-20

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PRIOR FILING DATE: 1998-03-20

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PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
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PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336

PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5% Score 21; DB 9; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGGTTCTCGATGAGAT 21.  
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DB 399 TTCGAGGTTCTCGATGAGAT 379

RESULT 26  
US-09-978-192A-482/C  
Sequence 482, Application US/09978192A  
Patent No. US2002017553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyere, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Pong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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 Query Match 95.5%; Score 21; DB 9; Length 3819;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Baker Kevin P.  
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 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Thomas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2630P1C63  
 CURRENT APPLICATION NUMBER: US/09/999,832A  
 PRIOR FILING DATE: 2001-10-24  
 PRIOR APPLICATION NUMBER: 09/918585  
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RESULT 27  
 US-09-999-832A-482/c  
 ; Sequence 482, Application US/09999832A  
 ; Publication No. US20020192706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

PRIOR APPLICATION NUMBER: 60/079786  
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Query Match 95.5%; Score 21; DB 9; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 399 TTGGAGTTCGATGAGAT 379

RESULT 28  
US-09-978-189-482/c  
Sequence 482, Application US/0978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman



APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Goddard, Audrey  
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APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCES: P2630P1C7  
CURRENT APPLICATION NUMBER: 'us/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29

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; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTGGAGTTCTCGATGGAGAT 21
DB      399 TTGGAGTTCTCGATGGAGAT 379

RESULT 29
US-09-978-608A-482/c
; Publication 482, Application US/09978608A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 482
; LENGTH: 3819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTGGAGTTCTCGATGGAGAT 21
DB      399 TTGGAGTTCTCGATGGAGAT 379

RESULT 30
US-09-978-585A-482/c
; Publication 482, Application US/09978585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm

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SEQ ID NO 482  
LENGTH: 3819  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-585A-482

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGGAGAT 21  
Db 399 TTGGAGTTCTCGATGGAGAT 379

RESULT 31  
US-09-978-191A-482/C  
Sequence 482, Application US/09978191A  
Publication No. US2003050239A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978, 191A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
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PRIOR FILING DATE: 1998-03-26  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22

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 PRIOR FILING DATE: 1998-04-22  
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 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;

Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTGGAGTTCTCGATGAGAT 21  
 Db 399 TTGGAGTTCTCGATGAGAT 379

RESULT 32  
 US-09-978-403A-482/c  
 Sequence 482, Application US/09978403A  
 Publication No. US20030050240A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deonoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P17  
 CURRENT APPLICATION NUMBER: US/09/978,403A  
 PRIOR FILING DATE: 2002-03-19  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
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 PRIOR FILING DATE: 1998-03-20

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PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
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PRIOR APPLICATION NUMBER: 60/084637  
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PRIOR APPLICATION NUMBER: 60/084639  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGGAGAT 21.  
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Db 399 TTGGAGTTCTCGATGGAGAT 379

RESULT 33  
US-09-978-564A-482/C  
Sequence 482, Application US/09978564A  
Publication No. US20030050241A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acid Encoding the Same  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-29



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PRIOR APPLICATION NUMBER: 60/083554

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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTTCGATGAGAT 21  
DB 399 TTGGAGTTTCGATGAGAT 379

RESULT 35  
US-09-981-915A-482/c  
Sequence 482, Application US/09981915A  
Publication No. US20030054986A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Saton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman



APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar U.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
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PRIOR APPLICATION NUMBER: 60/078936  
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PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105

PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-01  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity: 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCGATGAGAT 21  
Db 399 TTGGAGTTCGATGAGAT 379

RESULT 36  
US-09-978-824-482/c  
Sequence 482: Application US/09978824  
Publication No. US20030055216A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C14  
CURRENT FILING DATE: 2001-10-17  
PRIOR APPLICATION NUMBER: US/09/978,824  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327  
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PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
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PRIOR APPLICATION NUMBER: 60/084441

PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTTCGATGAGAT 21  
DB 399 TTCGAGTTTCGATGAGAT 379

RESULT 37  
US-09-918-585A-482/c  
Sequence 482, Application US/09918585A  
Publication No. US2003060406A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secretered and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/918,585A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
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PRIOR APPLICATION NUMBER: 60/081070

PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-15  
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Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0;

Qy 1 TTGGAGTCTCGATGAGAT 21  
Db 399 TTGGAGTCTCGATGAGAT 379

RESULT 38  
US-09-999-834A-482/c  
Sequence 482, Application US/09999834A  
Publication No. US20030064407A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Eileen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C75  
CURRENT APPLICATION NUMBER: US/09/999,834A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/081049  
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PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
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PRIOR APPLICATION NUMBER: 60/084414  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
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PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
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PRIOR APPLICATION NUMBER: 60/084643

PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query March 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCGAGTTCGATGAGAT 21  
DB 399 TTCGAGTTCGATGAGAT 379

RESULT 39  
US-09-978-423A-482/c  
Sequence 482, Application US/0978423A  
Publication No. US2003069178A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bocsetein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerilsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2650P1C21  
CURRENT APPLICATION NUMBER: US/09/978,423A  
CURRENT FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

1	PRIOR APPLICATION NUMBER: 60/064249
2	PRIOR FILING DATE: 1997-11-03
3	PRIOR APPLICATION NUMBER: 60/065311
4	PRIOR FILING DATE: 1997-11-13
5	PRIOR APPLICATION NUMBER: 60/066364
6	PRIOR FILING DATE: 1997-11-21
7	PRIOR APPLICATION NUMBER: 60/077450
8	PRIOR FILING DATE: 1998-03-10
9	PRIOR APPLICATION NUMBER: 60/077632
10	PRIOR FILING DATE: 1998-03-11
11	PRIOR APPLICATION NUMBER: 60/077641
12	PRIOR FILING DATE: 1998-03-11
13	PRIOR APPLICATION NUMBER: 60/077649
14	PRIOR FILING DATE: 1998-03-11
15	PRIOR APPLICATION NUMBER: 60/077791
16	PRIOR FILING DATE: 1998-03-12
17	PRIOR APPLICATION NUMBER: 60/078004
18	PRIOR FILING DATE: 1998-03-13
19	PRIOR APPLICATION NUMBER: 60/078686
20	PRIOR FILING DATE: 1998-03-20
21	PRIOR APPLICATION NUMBER: 60/078936
22	PRIOR FILING DATE: 1998-03-20
23	PRIOR APPLICATION NUMBER: 60/078930
24	PRIOR FILING DATE: 1998-03-20
25	PRIOR APPLICATION NUMBER: 60/078939
26	PRIOR FILING DATE: 1998-03-20
27	PRIOR APPLICATION NUMBER: 60/079294
28	PRIOR FILING DATE: 1998-03-25
29	PRIOR APPLICATION NUMBER: 60/079656
30	PRIOR FILING DATE: 1998-03-26
31	PRIOR APPLICATION NUMBER: 60/079664
32	PRIOR FILING DATE: 1998-03-27
33	PRIOR APPLICATION NUMBER: 60/079689
34	PRIOR FILING DATE: 1998-03-27
35	PRIOR APPLICATION NUMBER: 60/079683
36	PRIOR FILING DATE: 1998-03-27
37	PRIOR APPLICATION NUMBER: 60/079923
38	PRIOR FILING DATE: 1998-03-30
39	PRIOR APPLICATION NUMBER: 60/080105
40	PRIOR FILING DATE: 1998-03-31
41	PRIOR APPLICATION NUMBER: 60/080107
42	PRIOR FILING DATE: 1998-03-31
43	PRIOR APPLICATION NUMBER: 60/080165
44	PRIOR FILING DATE: 1998-03-31
45	PRIOR APPLICATION NUMBER: 60/080194
46	PRIOR FILING DATE: 1998-03-31
47	PRIOR APPLICATION NUMBER: 60/080327
48	PRIOR FILING DATE: 1998-04-01
49	PRIOR APPLICATION NUMBER: 60/080328
50	PRIOR FILING DATE: 1998-04-01
51	PRIOR APPLICATION NUMBER: 60/080333
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53	PRIOR APPLICATION NUMBER: 60/080334
54	PRIOR FILING DATE: 1998-04-01
55	PRIOR APPLICATION NUMBER: 60/081070
56	PRIOR FILING DATE: 1998-04-08
57	PRIOR APPLICATION NUMBER: 60/081049
58	PRIOR FILING DATE: 1998-04-08
59	PRIOR APPLICATION NUMBER: 60/081071
60	PRIOR FILING DATE: 1998-04-08
61	PRIOR APPLICATION NUMBER: 60/081195
62	PRIOR FILING DATE: 1998-04-08
63	PRIOR APPLICATION NUMBER: 60/081203
64	PRIOR FILING DATE: 1998-04-09
65	PRIOR APPLICATION NUMBER: 60/081229
66	PRIOR FILING DATE: 1998-04-09
67	PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819
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PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838
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PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27	PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083395
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05	PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084411
PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084633
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084634
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084635
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PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085323

PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTTCGATGAGAT 21  
Db 399 TTCCGAGTTCGATGAGAT 379

RESULT 40  
US-09-978-193A-482/c  
Sequence 482: Application US/0978193A  
Publication No. US20030073624A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fliviaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C6  
CURRENT APPLICATION NUMBER: US/09/978, 193A  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
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PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15



PRIOR APPLICATION NUMBER: 60/081838  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082568  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082569  
 PRIOR FILING DATE: 1998-04-21  
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 PRIOR FILING DATE: 1998-04-22  
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 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5% Score 21; DB 10; Length 3819;  
 Best Local Similarity 100.0%; Pred No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
 Db 399 TTGGAGTTCTCGATGAGAT 379

RESULT 41  
 US-09-999-830A-482/c  
 Sequence 482, Application US/09999830A  
 Publication No. US2003007700A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Batton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvarole, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerltsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Grimaldi, Paul J.  
 APPLICANT: Hillman, Austin L.  
 APPLICANT: Hillman, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoul, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tuma, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C70  
 CURRENT APPLICATION NUMBER: US/09/999,830A  
 CURRENT FILING DATE: 2001-08-31  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/077450  
 PRIOR FILING DATE: 1998-03-10  
 PRIOR APPLICATION NUMBER: 60/077632  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077641  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077649  
 PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085697  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 399 TTCGAGTTCTCGATGAGAT 379

## RESULT 42

US-09-978-757A-482/c  
Sequence 482, Application US/09978757A  
Publication No. US20030083248A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Nadler, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC26  
CURRENT APPLICATION NUMBER: US/09/978, 757A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
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PRIOR APPLICATION NUMBER: 60/079663  
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PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
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PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
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PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
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PRIOR APPLICATION NUMBER: 60/081955  
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PRIOR APPLICATION NUMBER: 60/081817  
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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
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PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22

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;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
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;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
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;; PRIOR FILING DATE: 1998-05-05  
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;; PRIOR APPLICATION NUMBER: 60/084441  
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;; PRIOR APPLICATION NUMBER: 60/084643  
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;; PRIOR FILING DATE: 1998-05-13  
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;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697  
;;  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCGAGTTCGATGAGAT 21

DB 399 TTCGAGTTCGATGAGAT 379  
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RESULT 43  
US-09-978-187B-482/c  
; Sequence 482, Application US/0978187B  
; Publication No. US20030096744A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geo, Wei-Qiang  
; APPLICANT: Geider, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC5  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
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; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR FILING DATE: 1998-03-12  
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; PRIOR FILING DATE: 1998-03-13  
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; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
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; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-03-25

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PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21  
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DB 399 TTCGAGTTCGATGAGAT 379

RESULT 44  
US-09-978-643A-482/c  
Sequence 482, Application US/09978643A

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/ Publication No. US20030104998A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C16
/ CURRENT APPLICATION NUMBER: US/09/978,643A
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 482
/ LENGTH: 3819
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-978-643A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
Db 399 TTCGAGTTCGATGAGAT 379

RESULT 45
US-09-978-375A-482/C
/ Sequence 482, Application US/09978375A
/ Publication No. US20030130181A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
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/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C24
/ CURRENT APPLICATION NUMBER: US/09/978,375A
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 482
/ LENGTH: 3819
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-978-375A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
Db 399 TTCGAGTTCGATGAGAT 379

RESULT 46
US-09-978-298A-482/C
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/ Publication No. US20030134785A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C2
/ CURRENT APPLICATION NUMBER: US/09/978,298A
/ NUMBER OF SEQ ID NOS: 60
/ Prior Application removed - See File Wrapper or Palm
/ Prior Filing Date: 2001-07-30
/ Prior Application Number: 60/062250
/ Prior Filing Date: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
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Db 399 TTGGAGTTCTCGATGAGAT 379

RESULT 47  
US-09-978-188A-482/C  
Sequence 482, Application US/09978188A  
Publication No. US20030139328A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P263091C8  
CURRENT APPLICATION NUMBER: US/09/978,188A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10  
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PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
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PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2, 1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCTCATGGAGAT 21  
DB 399 TTGGAGTTCTCATGGAGAT 379

RESULT 48  
US-09-978-681A-482/c  
Sequence 482, Application US/09978681A  
Publication No. US20030195148A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C18  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US/09/978, 681A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085697  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGAT 21  
Db 399 TTCGAGTTCTCGATGAGAT 379

RESULT 49  
US-09-978-194A-482/c  
Sequence 482, Application US/09978194A  
Publication No. US2003019533A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C10  
CURRENT APPLICATION NUMBER: US/09/978, 194A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
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PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR APPLICATION NUMBER: 60/081819  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-22

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 PRIOR APPLICATION NUMBER: 60/083392  
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 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083558  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083559  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083500  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083742  
 PRIOR FILING DATE: 1998-04-30  
 PRIOR APPLICATION NUMBER: 60/084366  
 PRIOR FILING DATE: 1998-05-05  
 PRIOR APPLICATION NUMBER: 60/084414  
 PRIOR FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/084441  
 PRIOR FILING DATE: 1998-05-06  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCGAGTTCTCGATGAGAT 21

Db 399 TTCGAGTTCTCGATGAGAT 379

RESULT 50  
 US-09-999-829A-482/c  
 Sequence 482, Application US/0999829A  
 Publication No. US20030195344A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gutney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Kijavini, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C61  
 CURRENT APPLICATION NUMBER: US/09/999, 829A  
 CURRENT FILING DATE: 2002-03-19  
 NUMBER OF SEQ ID NOS: 624  
 Prior Application removed - See File Wrapper or Palm  
 SEQ ID NO 482  
 LENGTH: 3819  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-999-829A-482

Query Match 95.5%; Score 21; DB 10; Length 3819;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 2, 2005, 01:34:12  
 Job time : 450 secs.

1 TTCGAGTTCTCGATGAGAT 21  
 399 TTCGAGTTCTCGATGAGAT 379